

FIGURE 1

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATG
AGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTTGGTGGT
TTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTT
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGG
TACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG
CTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAAA
TTAAACAAGGCTGGCCTTGTAAGTACTGAGTTGTTTAGGACTTTCTATTGTGGCAAACCTT
CCAGAAAAACAACCCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCAT
TATATATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTC
TTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTC
ATCAGTTTGCACAGTGGCAATTTTGGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGG
ACAAAGGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTT
GGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACA
TGGATTAAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCA
GAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACT
GATGAATGCTGATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATCTAAAGGATATCAT
CAAGAAGACTATTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACT
ATG

FIGURE 2

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV
LCIATIVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFG
MGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSSVLHSGNFGTDLEQKLHW
NPEDKGYVLHMITTAAEWSMSFSFFGFFLT YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR
LLSRDI

Important features:

Type II transmembrane domain:

amino acids 13-33

Other Transmembrane domains:

amino acids 54-73, 94-113, 160-180, 122-141

N-myristoylation sites.

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACC
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGTGGCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTC
CTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTG
GATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTAAAGACTATGAGATACGTCAGTATGTTGTACAG
GTGATCTTCTCCGTGACGTTTGCATTTTCTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGG
AGTATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGAATCTGCTGATCCTGG
TTTTCATGGTGCCTTTTACATTGGCTATTTATTGTGAGCAATATCCGACTACTGCATAAACAACGA
CTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTCTGGAAACTAGGAGATCCCTTTCC
CATTCTCAGCCCAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAG
TGACTCTCATGGCTCTTCTTTCTGGATTTGGTGTGTCAACTGCCCATACACTTACATGCTTACTTC
CTCAGGAATGTGACTGACACGGATATTCTAGCCTGGAACGGCGACTGTGCAAACCATGGATATGAT
CATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACA
AACCATCAGGTTTCTGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAAAATCTTACT
CTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCT
ATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTCAAGGGGAAATATTTTAATTTTCTTGGTT
ACTTTTTCTCTATTTACTGTGTTTGGAAAATTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTT
GGGAAAACGGATCCTGTCACAAGAGGCATTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGT
GAAGTTTGGTCCCAACACATTTCTTTCATTCTGTGTTGGAATAATCATCGTCACATCCATCAGAGGAT
TGCTGATCACTCTTACCAAGTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTG
CTATTAGCACAGATAATGGGCATGACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTT
AGAATACCGCACCATTAATCACTGAAGTCCTTGGGAACTGCAGTTCAACTTCTATCACCGTTGGTTTG
ATGTGATCTTCTGTCAGCGCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCA
GAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTA
GATATAAGAGGGGGGAAAATGGAACAGGGCCTGACATTTTATAAACAACAAAATGCTATGGTAGC
ATTTTTCACCTTCATAGCATACTCCTTCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAG
AACATGAGAGGGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGG
TGTAGAGGCGGAGAGGAGCCAAGAACTAAAGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGT
CTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTGG
CCTTGAGATTGACTCATTAATAACAGAGACTGTAACAAAAAAGGGCGCCGCG
ACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTGTCAGCTTATAATG

FIGURE 4

MSFLIDSSIMITSQILFFGFGWLFMRQLFKDYEIRQYVVQVIFSVTFASFCTMFELIIFEILGV
LNSSSRYPFHWMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDP
FPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQ
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDLEELSRQ
LFLETADLYATKERIEYSKTFKGKYFNFELGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGY
FVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 5

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGTTCC
 AGAATCTCCATCCGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATCTGAGGT
 GTTTCCTCGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTGCTTCTCACT
 TCCATCTGGACCAGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCTTCCATCCAGGT
 GTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCAGCAGCTGAATTTACAG
 AAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGCCCGCAAGGACCAAGTTGAAACAGCC
 TTGAAAGCTAGCTTTGAACTTGACAGCTATGGCTGGGTTGGAGATGGATTCTGCTCATCTCTAG
 GATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGTGGGTGCTCTGATTGGAAGGTTCAGTGA
 GCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA
 ATTATCACCACCAAGATCCCATATTCAACACTCAAACGCAACACAACAGAAATTTATGTT
 CAGTGACAGTACCTACTCGGTGGCATCCCCCTTACTCTACAATACCTGCCCCCTACTACTCCTC
 CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAATGATTTGTGTACAGAAGTTTTTATG
 GAACTAGCACCATGTCTACAGAACTGAACCATTTGTTGAAAATAAAGCAGCATCAAGAATGA
 AGCTGCTGGGTTTGGAGGTGTCCCCACGGCTCTGCTAGTGTGCTCTCCTCTTCTTGGTGTG
 CAGCTGGTCTTGGATTGCTATGTCAAAGGTATGTGAAGGCCTTCCTTTTACAACAAGAAAT
 CAGCAGAAGGAAATGATCGAAACCAAGTAGTAAGGAGGAGAAGGCCAATGATAGCAACCTAA
 TGAGGAATCAAAGAAAACCTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGC
 GATGCCCTGGAAGCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTT
 CATGCTCCTTACCTGCCCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCA
 CCCTTGGTTCTTAACCTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT
 GCCCTTCTCCTTATGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCCT
 TTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGCAAAGTGCAAGGAC
 CTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCCTGGCTGTCTGAGGCTAGGTGGGTG
 AAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGACCCCTTCTTCA
 GCTCTGAAAGAGAAACACGTATCCACCTGACATGTCTTCTGAGCCCGGTAAAGAGCAAAAGAAAT
 GGCAGAAAAGTTTAGCCCCGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTCTGTAAA
 GCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACTGTCAGCAGGGACTGTAAAC
 ACAGACAGGGTCAAAGTGTTTCTCTGAACACATTGAGTTGGAATCACTGTTTGAACACACACA
 CTTACTTTTTCTGGTCTCTACCCTGCTGATATTTCTCTAGGAAATATACTTTTACAAGTAACA
 AAAATAAAAACCTCTATAAATTTCTATTTTATCTGAGTTACAGAAATGATTACTAAGGAAGATT
 ACTCAGTAATTTGTTTAAAAAGTAATAAAATTCACAAACATTTGCTGAATAGCTACTATATGTC
 AAGTGTGTGCAAGGTATTACACTCTGTAATTGAATATTATTCCTCAAAAAATTGCACATAGTAG
 AACGCTATCTGGGAAGCTATTTTTTTCAGTTTTGATATTTCTAGCTTATCTACTTCCAACTAAT
 TTTTATTTTTGCTGAGACTAATCTTATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATT
 TATTATTAACATACCTAAGAAGTACATTGTTACCTCTATATACCAAGCACATTTTAAAGTGCC
 ATTAACAAATGTATCACTAGCCCTCCTTTTCCAAACAAGAAGGGACTGAGAGATGCAGAAATATT
 TGTGACAAAAAATTAAAGCATTTAGAAAACCTT

FIGURE 6

MARCFSLVLLLSIWTTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG
LSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYN
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPAPASTSIPR
RKKLICVTEVFMETSTMSTETEPFVENKAAFNEAAGFGGVPTALLVLALLFFGAAAGLGFCYVK
RYVKAFFFTNKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSPSKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 7

CGCCGCGCTCCCGCACCCGCGGCCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCCGG
GGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCCGCCCCGCAGCGCAACTCGGTCCAGTCGGGGCGG
CGGCTGCGGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCCTGCTGCTGGCGG
CGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGTCCAGTCAAGCCCGGCCCG
GCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGAGGTTGAGGAACTGAT
GGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGCTA
AAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTATCACAATGAGACCAACACAGAC
ACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAATTCACAAGATAACCAACACAGAC
TGGACAAATGGTCTTTTCAGAGACAGTTATCACAATCTGTGGGAGACGAAGAAGGCAGAAGGAGCC
ACGAGTGCATCATCGACGAGGACTGTGGGCCCAGCATGTACTGCCAGTTTGCCAGCTTCCAGTAC
ACCTGCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAGTGTGTGGAGACCA
GCTGTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGCAGCAATGGGACCATCTGTGACA
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCCTTCCAGAGAGGCTGCTGTTCCTGTGTGC
ACACCCTGCCCGTGGAGGGCGAGCTTGGCAATGACCCCGCCAGCCGGCTTCTGGACCTCATCAC
CTGGGAGCTAGAGCCTGATGGAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGC
CCCACAGCCACAGCCTGGTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGG
GAGATCCTGCTGCCAGAGAGGTCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCG
CCAGGAGCTGGAGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCCGCTG
CCGCCCTGCACCTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATAGTGC
TAGAAATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCTTA
CATCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTAGCT
CCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAACTGCA
GGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAGACAGCCG
TTTGTCTACATGGCTTTTGATAATTGTTTGGGGGAGGAGATGGAAACAATGTGGAGTCTCCCTC
TGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCCTGCTTTGCAAACATCAACCTGGCAAAATG
CAACAAATGAATTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTGTGCCTTCAGCTGTTGC
AGATGAAATGTTCTGTTTACCCTGCATTACATGTGTTTATTCATCCAGCAGTGTGCTCAGCTCC
TACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTCCCTCTCTCAGCACAGCCTGGGG
AGGGGTCATTGTTCTCCTCGTCCATCAGGGATCTCAGAGGCTCAGAGACTGCAAGCTGCTTGCC
CAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCATCTGGTTGTGACTCTAAGCTCAGTGCTCT
CTCCACTACCCACACCAGCCTTGGTGCCACCAAAAGTGCTCCCCAAAAGGAAGGAGAATGGGAT
TTTCTTGAGGCATGCACATCTGGAATTAAGGTCAAACCTAATCTCACATCCCTCTAAAAGTAAA
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGCAGCCGTCTTCTAATGAAGACAATGAT
ATTGACACTGTCCCTCTTTGGCAGTTGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCA
TACAGGTTAACCAGCAAAACAGTACTTAGGTAAATGTAGGCGGAGGATTATAAATGAAATTTGC
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGC
TGTGTGAAACATGGTTGTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATG
TTTTAGGTGTGATGAGTGTGTCACCATGTATTCTCCAGAGTTCCTAAAGTTAAAGTTGCA
CATGATTGTATAAGCATGCTTTCTTTGAGTTTAAATTTATGTATAAACATAAGTTGCATTTAGAA
ATCAAGCATAAATCACTTCACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 8

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGFALSYQEEATLNEMFREVEELMEDTQHKL
RSAVEEMEAEAAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTGQMVFSE
TVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRLCTR DSECCGDQLCVWGH
TKMATRGSNGTICDNQRDCQPGLCFAFQRLFPVCTPLPVEGELCHDFASRLLDLITWELEPDG
ALDRPCASGLLCQPHSHSLVYVCKPTFVGSRDQGEILLPREVPDEYEVGSFMEEVRQELEDLE
RSLTEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 9

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCCAC
GGCCCACCTTGTGAACTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCATCCAAAG
GCCTAATCCAACGTCTGTCTTCAATCTGCAAATCTATGGGGTCTGGGGCTCTTCTGGACCCCT
AACTGGGTACTGGCCCTGGGCCAATGCGTCCTCGCTGGAGCCTTTGCCTCCTTCTACTGGGCCTT
CCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCCGCACACTCCGTTACC
ACACTGGGTCAATGGCATTGAGGCCCTCATCTGACCCCTGTGCAGATAGCCCGGGTCATCTTG
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGCCCGCTGCATCATGTGCTGTTT
CAAGTGTGCTCTGCTGTCTGGAAAAATTATCAAGTTCCTAAACCGCAATGCATACATCATGA
TCGCCATCTACGGGAAGAATTCTGTGTCTCAGCCAAAAATGCGTTCATGTACTCATGCGAAAC
ATTGTGAGGGTGGTCGTCCTGGACAAAGTCACAGACCTGCTGCTGTTCTTTGGGAAGCTGCTGGT
GGTCGGAGGCGTGGGGTCTGTCTTCTTTTTTTCTCCGGTCGCATCCCGGGGCTGGGTAAAG
ACTTTAAGAGCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCCTGGGGGCCTAT
GTCATCGCCAGCGGCTTCTTCAGCGTTTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTT
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAA
AGATTCTGGGCAAGAAGAACGAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGACAGCTCCGG
CCCTGATCCAGGACTGCACCCCAACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGT
CTCCATTTTGTGGTAAAAAAGGTTTTAGGCCAGGCGCGGTGGCTCACGCCTGTAATCCAACACT
TTGAGAGGCTGAGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTG
AAACCTCCGTCTCTATTAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCCA
GCTACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCGGGAGGCAGAGTTGCAGTGAGCCGA
GATCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
AAGATTTTATTAAAGATATTTTGTTAACTC

FIGURE 10

RTRGRTRGGCEKVPINTSCNPHTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVLGLEFWTL
NWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAKNAFMLLMRN
IVRVVVLDKVTDLLLLFFGKLLVVGGVGVLSFFFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLKILGKKNEAPPDNKKRKK

Important features:

Transmembrane domains:

amino acids 57-80 (type II), 110-126, 215-231, 254-274

N-glycosylation sites.

amino acids 16-20, 27-31, 289-293

Hypothetical YBR002c family proteins.

amino acids 276-288

Ammonium transporters proteins.

amino acids 204-231

N-myristoylation sites.

amino acids 60-66, 78-84

Amidation site.

amino acids 306-310

FIGURE 11

GCCCCGCGCCCGGCGCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAGCCTGC
TCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCTGCTGCCCGC
CAGCCGCAACTCCACCGTGAGCGCCTCATCTCACGTTCTTCTCTTCTGCGGGTGCTGGTGTCCA
TCATTATGCTGAGCCCGGCGTGAGAGTCTACAAGCTGCCCTGGGTGTGTGAGGAGGGGGC
GGGATCCCCACCGTCTGCAGGGCCACATCGACTGTGGCTCCCTGCTTGGCTACCGCGCTGTCTACCG
CATGTGCTTCGCCACGGCGGCTTCTTCTTCTTTTTCACCTGCTCATGCTCTGCGTGAGCAGCA
GCCGGGACCCCCGGGCTGCCATCCAGAATGGGTTTGGTCTTTAAGTTCTGATCCTGGTGGGCTC
ACCGTGGGTGCCTTCTACATCCCTGACGGCTCCTTACCAACATCTGGTTCTACTTCGGCGTGTGGG
CTCCTTCTCTTCATCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCCTGGAACAGCGGT
GGCTGGGCAAGGCCGAGGAGTGCATTCCCGTGCCTGGTACGCGAGGCTCTTCTTCTCACTCTCCTC
TTCTACTTGCTGTCGATCGCGCGCTGGCGCTGATGTTTACTTACTGAGCCAGCGGCTGCCA
CGAGGCAAGGTCTTCATCAGCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGTC
CCAAGGTCCAGGACGCCAGGCCAAGTCCGGTCTGCTGCAGGCTCGGTATCACCTCTACACCATG
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCATTTGCCAACCCAGCT
GGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCGAGCATTG
TGGGCTCATCATCTTCTCTGTGCACCTCTTCATCAGTCTGCGCTCCTCAGACCACCGGCAGGTG
AACAGCCTGATGCAGACCGAGGAGTGGCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGT
GGCAGCCTGTGAGGGCCGGGCTTTGACAACGAGCAGGACGGGCTCACCTACAGCTACTCTTCTTCC
ACTTCTGCCTGGTGTGGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAG
ACCCGGAAGATGATCAGCACGTGGACCGCGGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCT
CCTCTACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGAGCCTCA
CAGCTGCCATCTGGTGCCTCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTC
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCTGAGCCGGGC
CTTCTAGTCGTAGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCAC
ACCCACACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCTGTTGCCATACTCAGCATCTCGGATGAA
AGGGCTCCCTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGAACTCCCACCACAG
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCAGGGGACCCTGCCCCCTTCTGT
GACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCCTGTAAAAAAA

FIGURE 12

MGACLGACSLSCASCSCGAPCILCSCCPASRNSTVSRIFTFFFLGVLVSIIMLSPGVESQL
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRDPRAAIQ
NGFWFFKFLILVGLTVGAFYIPDGSTNIWFYFGVVGSLFLILIQVLVLLIDFAHSWNQRWLKAE
ECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVSIAAVLPKV
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI
VGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQVAACEGRAFDNEQDGVTSY
SFFHFCLVLASLHVMTLTNWKPGETRKMISTWTAVVVKICASWAGLLLYLWTLVAPLLLRNRD
FS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 13

CGGGCCAGCCTGGGGCGGGCCGGCCAGGAACCCCGTTAAGGTGTCCTCTCTTTAGGGATGGTGA
GGTTGGAAAAAGACTCCTGTAACCTCCTCCAGGATGAACCACTGCCAGAAGACATGGAGAACG
CTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCACACAA
CTCATGGCCAGGATTGAGTCTATGAAGGAAGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC
TTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATAGAGTTAAATG
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTACTATTCTTCATAT
TTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCATATGCTGTGTGCAG
ACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTTTACTAGCAAAAG
TGATCCTTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTGCCCATCATTTTCATTCATC
CTTGCTGGATTGAGACGTGGTTCTCGGATTTCAAAGTGTTACCTCAAGAAGCAGAAGAAGAAAA
CAGACTCCTGATAGTTTCAAGATGCTTCAAGAGGGCAGCACTTATACCTGGTGGTCTTTCTGATG
GTCAGTTTATTTCCCTCCTGAATCCGAAGCAGGATCTGAAGAAGCTGAAGAAAAACAGGACAGT
GAGAAACCACTTTTAGAAGTATGAGTACTACTTTTGTAAATGTGAAAAACCTCACAGAAAGTC
ATCGAGGCAAAAAGAGGCAGGAGTGGAGTCTCCCTGTGACAGTAAAGTTGAAATGGTGACGTC
CACTGCTGGCTTTATTGAACAGCTAATAAAGATTATTTATTGTAATACCTCACAAACGTTGTAC
CATATCCATGCACATTTAGTTGCCTGCCTGTGGCTGGTAAGGTAATGTCATGATTCATCCTCTCT
TCAGTGAGACTGAGCCTGATGTGTTAACAATAGGTGAAGAAAGTCTTGTGCTGTATTCCTAATC
AAAAGACTTAATATATTGAAGTAACACTTTTTTAGTAAGCAAGATACCTTTTTATTTCAATTAC
AGAATGGAATTTTTTGTTCATGTCTCAGATTTATTTGTATTTCTTTTTTAACACTCTACATT
TCCCTTGTTTTTAACTCATGCACATGTGCTCTTGTACAGTTTTAAAAAGTGAATAAAATCTG
ACATGTCAATGTGGCTAGTTTTATTTTCTTGTGTTTGCATTATGTGTATGGCCTGAAGTGTGGGA
CTTGCAAAAGGGGAAGAAAGGAATTGCGAATACATGTAAATGTCAACAGACATTGTATTATTT
TTATCATGAAATCATGTTTTTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTGAATGC
ACAAAATGACTTAAACCATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAA
CTAAATTAAAAA

FIGURE 14

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDLLF
VTLWIIELNVNGGIENTLEKEVMQYDYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIALTT
AVTSAFLLAKVILSKLFSQGAFGYVLPISFILAWIETWFLDFKVLQPQAEENRLLIVQDASER
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 15

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCGCCAGGAAAGACTGAGG
CCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCGCCGCTCCCGGGACAGAAGATGCTGCCAG
GGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGCAGGGCTGCCCAT
CCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGGACACGGTGCCC
CGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGC
AGGCAGCTTTGCCGGCCTGCCGGCCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCC
TGCCAGCGGGGTCTTCCAGCCACTCGCCAACCTCAGCAACCTGGACCTGACGGCCAACAGGCTG
CATGAAATCACCAATGAGACCTTCCGTGGCCTGCGGCGCCTCGAGCGCCTCTACCTGGGCAAGAA
CCGCATCCGCCACATCCAGCCTGGTGCTTCGACACGCTCGACCGCTCCTGGAGCTCAAGCTGC
AGGACAACGAGCTGCGGGCACTGCCCCGCTGCGCCTGCCCGCCTGCTGCTGCTGGACCTCAGC
CACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCT
GGCTGCTTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACC
TGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCTCCGGGGCCTGACG
CGCCTGCGGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCGCAGGACCTGGCCGGCTGGC
TGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCC
TCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCGCTGAGC
TGGTTTGGCCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCA
CTTCCCGCCCAAGAAGCTGGCCGGTGTCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAG
CCACCACCACACAGCCACAGTGGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGCCTTGTCT
TCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTC
CACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCA
ATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGCTTGTGCCCGAAGGCTTCACG
GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAG
GCCACCACGGTCCCTGACCTGGGCATCGAGCCGGTGAGCCCACTCCCTGCGCGTGGGGCTGC
AGCGCTACCTCCAGGGGAGTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCG
GGCCCTGATAAGCGGTGGTGACGTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCA
GCTGCGGCCCAACGCCACTTACTCCGTCTGTGTATGCCCTTGGGGCCCGGGCGGGTGCCGGAGG
GCGAGGAGGCCTGCGGGGAGGCCATACACCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGC
GCTGGCTGCGGTGGGGGACGCTTACTGTGTGCGCGGGGGCGGGCCATGGCAGCAGCGGCTCAGG
ACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCCTTGGAG
CCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGAGTGTGAGGTGCC
ACTCATGGGCTTCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAGCCCTACATCTAAGCCA
GAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCC
ACACCACGTAAGTTCTCAGTCCCAACCTCGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCT
GGGCCCTGTTCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCC
CTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTC
CCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCAC
TCCAGGCGGACCTTGGGGGCCAGTGAAGGAAGCTCCCGGAAGAGCAGAGGGAGAGCGGGTAGGC
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGAAGATGC
TTTAGGAACATGTTTGTCTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCT
GGGAAGATGTTTTCAAACTCAGAGACAAGGACTTTGGTTTTGTAGACAAACGATGATATGAA
GGCCTTTTGTAGAAAAAATAAAGATGAAGTGTGAA

FIGURE 16

MCSRVP LLLPL LLL L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F E N G I T
M L D A G S F A G L P G L Q L L D L S Q N Q I A S L P S G V F Q P L A N L S N L D L T A N R L H E I T N E T F R G L R R L E R L Y
L G K N R I R H I Q P G A F D T L D R L L E L K L Q D N E L R A L P P L R L P R L L L L D L S H N S L L A L E P G I L D T A N V E
A L R L A G L G L Q Q L D E G L F S R L R N L H D L D V S D N Q L E R V P P V I R G L R G L T R L R L A G N T R I A Q L R P E D L
A G L A A L Q E L D V S N L S L Q A L P G D L S G L F P R L R L L A A A R N P F N C V C P L S W F G P W V R E S H V T L A S P E E
T R C H F P P K N A G R L L L E L D Y A D F G C P A T T T T A T V P T T R P V V R E P T A L S S S L A P T W L S P T A P A T E A P
S P P S T A P P T V G P V P Q P Q D C P P S T C L N G G T C H L G T R H H L A C L C P E G F T G L Y C E S Q M G Q G T R P S P T P
V T P R P P R S L T L G I E P V S P T S L R V G L Q R Y L Q G S S V Q L R S L R L T Y R N L S G P D K R L V T L R L P A S L A E Y
T V T Q L R P N A T Y S V C V M P L G P G R V P E G E E A C G E A H T P P A V H S N H A P V T Q A R E G N L P L L I A P A L A A V
L L A A L A A V G A A Y C V R R G R A M A A A A Q D K G Q V G P G A G P L E L E G V K V P L E P G P K A T E G G E A L P S G S E
C E V P L M G F P G P G L Q S P L H A K P Y I

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 579-599

EGF-like domain cysteine pattern signature.

amino acids 430-442

Leucine zipper pattern.

amino acids 197-219, 269-291

N-glycosylation sites.

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

Tyrosine kinase phosphorylation sites.

amino acids 124-131, 337-345

N-myristoylation sites.

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,
594-600, 640-646

FIGURE 17

GCAGCGGCGAGGCGGCGGTGGTGGCTGAGTCCGTGGTGGCAGAGGCGAAGGCGACAGCTCATGCG
GGTCCGGATAGGGCTGACGCTGCTGCTGTGTGCGGTGCTGCTGAGCTTGGCCTCGGCGTCCCTCGG
ATGAAGAAGGCAGCCAGGATGAATCCTTAGATTCCAAGACTACTTTGACATCAGATGAGTCAGTA
AAGGACCATACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTTCTTGATTGAGAAGAATCTGA
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGAAAAGTGTACAG
AAGATATCAGCTTCTAGAGTCTCCAAATCCAGAAAACAAGGACTATGAAGAGCCAAAGAAAGTA
CGGAAACCAGCTTTGACCGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTTTCT
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGGAGGGAAGATGGCAGACTGTGGTGTG
CTACAACCTATGACTACAAAGCAGATGAAAAGTGGGGCTTTTGTGAAACTGAAGAAGAGGCTGCT
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAATGAAAATCCTTAATGGAAG
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA
CCAAAGCCCTGGAGAGAGTGTATATGCTCTTTTATTTGGTGATTACTTGCCACAGAATATCCAG
GCAGCGAGAGAGATGTTTGAAGCTGACTGAGGAAGGCTCTCCCAAGGGACAGACTGCTCTTGG
CTTTCTGTATGCCTCTGGACTTGGTGTTAATTCAAGTCAGGCAAAGGCTCTTGTATATTATACAT
TTGGAGCTCTTGGGGCAATCTAATAGCCACATGGTTTTTGGTAAGTAGACTTTAGTGGAAGGCT
AATAATATTAACATCAGAAGAATTTGTGGTTTATAGCGGCCACAACTTTTTCAGCTTTCATGATC
CAGATTTGCTTGTATTAAGACCAAATATTCAGTTGAACTTCCTTCAAATTCTTGTTAATGGATAT
AACACATGGAATCTACATGTAAATGAAAGTTGGTGGAGTCCACAATTTTCTTTAAATGATTAG
TTTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAATGGCTCTTTTAAATTTTCTCTGAGTTG
GAATTGTCAGAATCATTTTTACATTAGATTATCATAATTTAAAAATTTTCTTTAGTTTTTCA
AAATTTTGTAATGGTGGCTATAGAAAAACAACATGAAATATTATACAATATTTTGCAACAATGC
CCTAAGAATTGTTAAATTCATGGAGTTATTTGTGCAGAATGACTCCAGAGAGCTCTACTTTCTG
TTTTTTACTTTTCATGATTGGCTGTCTTCCATTATTCTGGTCATTTATTGCTAGTGACACTGT
GCCTGCTTCCAGTAGTCTCATTTTCCCTATTTTGCTAATTTGTTACTTTTCTTTGCTAATTTGG
AAGATTAACTCATTTTTAATAAAATTATGTCTAAGATTAAAAAAAAAAAAAAAAAAAAAAAAA
AA

FIGURE 18

MRVRIGLTLLLCAVLLSLASASSDEEGSQDES LDSKTTLTSDSVKDHTTAGRVVAGQIFLDSESEL
ESSIQEEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHGEPCHFPLFLDK
EYDECTSDGREDGRLWCATTYDYKADEKWGFCETEEEAARRMQEAEMMYQTGMKILNGSNKKSQKR
EAYRYLQKAASMNHTKALERSYALLFGDYLPQNIQAAREMFELTEEGSPKGQTALGFLYASGLGVN
SSQAKALVYYTFGALGGNLIAMVLVSRL

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 195-199, 217-221, 272-276

Tyrosine kinase phosphorylation site.

amino acids 220-228

N-myristoylation sites.

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

Glycosaminoglycan attachment site.

amino acids 267-271

Microbodies C-terminal targeting signal.

amino acids 299-303

Type II fibronectin collagen-binding domain protein.

amino acids 127-169

Fructose-bisphosphate aldolase class-II protein.

amino acids 101-119

FIGURE 19

AATTCAGATTTTAAGCCCATTCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTT
GTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGG
CCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAACTAAAGATTGAAGACATCACTG
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCCAGAACCTTTTGAT
AAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAACAGCTTTAAAGGCAGA
AACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG
CCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGTCTCTGGGGTCTGATCAATAATGCTGGTGTT
CCCGCGTGCTGGCTCCCAGTACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA
CCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAG
TTATTAATGTCTCCAGTGTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAA
TATGCAGTGAAGGTTTCAATGACAGCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTC
ATGCATTGAACCAGGATTGTTCAAAACAACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAC
TCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAACAACAATATGGAGAAGGTTACATTGAAAA
AGTCTAGACAAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTG
CATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAA
GCAGAGCTGGCTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGA
AATTGGCCGATTTCAAGAACACATCTCCTTTTCAACCCATTCTTATCTGCTCCAACCTGGACT
CATTTAGATCGTGCTTATTTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGT
CCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCT
GTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTTGCCCATTCAAATGA
TCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGTTAAGT
ATCATCTCTTATCTAAATATTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 20

MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESG
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDWLTLEDY
REPIEVNLFGLISVTLNMLPLVKKQQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMK
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEGYIEKSLDKLKGNKSYVNMD
LSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQKAELANPKAV

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 21

CTGAGGCGGCGGTAGCAATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCG
CACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAAGTAAAA
GGTGAAGCCAAGAACAGCATTACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGA
CATTGAGAAATATATTCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATG
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGTTGGTACAAATCCGT
CGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAACTTCAGGAGCATT
TTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTCTACTC
ATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTCACAGGGTACCTTTAGTGGTT
GCCAATCTGGGCATGTCTGAACAACGCGTTATAAACTGTATCAGGTTCTGTATGTCCACTGG
TTTTAGCCGAGCAGTACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGG
TACATAAGATAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG
GAAGACAGTGAACAAGCAGTAGATAAACTAGTAAAGGATGTAAACAGATTAAACGAGAAATTGA
GAAAAGGAGAGGAGCAGATTGAGGAGCAAGAGAGAAGAACATCCAAAAGACCCCTCAGGAGA
ACATTTTTCTTTGTGAGGCATTACGGACCTTTTTTCCAAATCTGAATTTCTTCATTGATGTT
ATGTC'TTTAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACTACAACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAGCTAGTCCAGCTAGTACACCAC
AAATCATTAAGCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTA
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAT
GAGCAGCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTC
CTACATTTTGATCCTTTTAACTTACAAGGAGATTTTTTATTTGGCTGATGGGTAAAGCCAAAC
ATTTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTACC
TGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAACATCA
GATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAG
ACACATTCTTTAGAATTGGAAGAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT
TAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATT
GAGACCATGTCTATTAAAAATAAAATGGAAGCAAGAATAGCCTTATTTCAAATATGGAAA
GAAATTTATATGAAAATTTATCTGAGTCATTAAATTTCTCCTTAAGTGATACTTTTTTAGAAGTA
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAAATTTGCAAAACATCATCT
AAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIIDIQKYI
PCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL
VFLLLTPSIITESCSTHRLHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSSRAV
QTHSSKFEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA
QIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL
MVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQDKRSKANTGSSNQDKASKMSSPET
DEEIEKMKGFGEYSRSPTE

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation sites.

amino acids 75-79, 322-326

N-myristoylation site.

amino acids 184-154

Growth factor and cytokines receptors family.

amino acids 134-150

FIGURE 23

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCGAGCGCAGGGCAGCCCAA
GCAGCGCGCAGCGAACGCCCGCGCGCCACACCCCTCTGCGGTCCCGCGGGCGCTGCCACCCCTCCCTCCTTCCCC
GCGTCCCCGCTCGCGGCCAGTCAGCTTGCCGGGTTGCTGCCCGCGAAACCCCGAGGTCAACAGCCCGCGCTCT
GCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGCGCTGGCACCGGGGACCGTTGCCTGA
CGCGAGGCCAGCTCTACTTTTCGCCCGCGCTCTCCTCCGCTGCTCGCTCTTCCACCAACTCCAACCTCCTTCTCC
TCCAGTCCACTCGCTAGTCCCCGACTCCGCGAGCCCTCGGCCCGCTGCCGTAGCGCGCTTCCCGTCCGGTCCCAAA
GGTGGGAACGCGTCCGCCCGCGCCGACCAATGGCACGGTTCGGCTTGCCCGCGCTTCTCTGCACCCTGGCAGTGCTC
AGCGCGCGCTGCTGGTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGGACGCTTTACGTGTCCAAAGGCTTC
AACAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATCTGTCCCGAGGGTCTACCTGCTGCTCT
CAAGAGATGGAGGAGAAGTACAGCTGCAAGTAAAGATGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTG
CAAGCTGTCTTTGCTTACGTTACAAGAAGTTGATGAATTCTCAAAGAATACTTGAATAATGCAGAGAAATCCCTG
AATGATATGTTTGTGAACATATGGCCATTATACATGCAAAATCTGAGCTATTTAAAGATCTCTTCTAGAGTTG
AAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAAATGCTAAATGACTTCTGGGTCGCTCCTGGAGCGGATG
TTCCGCTGCTGAACCTCCAGTACCCTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAG
CCCTTCGGAGATGTCCCTCGCAAATTGAAGCTCCAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTCGCTCAAGGC
TTAGCGGTTCGGGAGATGTCTGAGCAAGGTCTCCGTGGTAAACCCACAGCCAGGTGTACCCATGCCCTGTTGAAG
ATGATCTACTGCTCCCACTGCCGGGTCTCGTACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGC
TGTTTGGCCAAACAGGGGATCTCGATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTA
GAGGGTCCCTTTCAACATTGAATCGGTGATGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGAT
AATAGTGTTCAGTGTCTCAGAAGGTTTCCAGGGATGTGGACCCCAAGCCCTCCAGCTGGACGAATTTCTCGT
TCCATCTCTGAAAGTGCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACACAGCAGCTGGCACT
AGTTTGGACCGACTGGTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGGTCTCCTCCTTCCGAGCAAC
GTTTGAACGATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTAC
CTGTTTGAGTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACACAGAC
ATACTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACAGCAAGATGAAGAATGCATACAATGGGAACGAGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCAGAG
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTGGGGCA
CAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTTCTCAAACCTGAG
AAAAAGTGTTCATCAAAAAGTTAAAGGCACCACTTATCACTTTTCTACCATCCTAGTGACTTTGCTTTTAAATGAA
TGACAAACATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTCTCATTCACTTTTGGG
AGGAAAGGGAGCTGTGATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCTAACAGTGTAGGTACAGAA
CTATAGTTAGTTGTGATTGTTGATTTTATCACTCTATTATTGTTTGTATGTTTTTCTCATTTCGTTTGTGGGTT
TTTTTTTCCAACGTGTGATCTCGCTTGTTCCTTACAAGCAACAGGGTCCCTTCTGGCACGTAACATGTACGTATT
TCTGAAATATTAATAGCTGTACAGAAGCAGGTTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 24

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFKNKDAPLHEINGDHLKICPQGST
CCSQEMEKEYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSINDMFVKTYGH
LYMQNSELFKDLFVELKRYVVGVNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTE
QLKPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGL
VTVKPCYNYCSNIMRGCLANQGDLDFFWNNFIDAMLMVAERLEGPFNIESVMDPIDVKISDAIMN
MQDNSVQVSQKVFQGCPPKPLPAGRISRSISESAFSARFRPHHPEERPTTAAGTSLDRLVTDVK
EKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNEVQVDT
KPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG
KSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

Important features:

Signal peptide:

amino acids 1-22

ATP/GTP-binding site motif A (P-loop).

amino acids 515-524

N-glycosylation site.

amino acids 514-518

Glycosaminoglycan attachment sites.

amino acids 494-498, 498-502

N-myristoylation sites.

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

Glypicans proteins.

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

FIGURE 25

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC
CTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACT
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAA
TGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTGCGCAGAGGCCACAGGGACCGAGGC
CAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAAAGATTGGTTTCCTGAG
AGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGTGCCCTGTGATCATT
TCAAGGGCAATGTGAAGAAAACAAGACACCAAGGCACCACAGAAAGCCAAACAAGCATTCCAGA
GCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTGCTCTGCCTTTGTAGGAGCTCTG
AGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTC
TTCTTCTCCCACTCACTCTCCCACTGTACCCACCCCTAATCATTCCAGTGCTCTCAAAAAGCA
TGTTTTTCAAGATCATTTTGTGTTGTGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCT
GTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCT
AGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTT
AAATGTCAAAAAAAAAAAAAAAAA

FIGURE 26

MKVLISL L L L L L P L M L M S V S S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R K F M
T V S G L P K K Q C P C D H F K G N V K K T R H Q R H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

Important features:

Signal peptide:

amino acids 1-22

N-myristoylation sites.

amino acids 27-33, 46-52

FIGURE 27

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAG
AGCTGGTCTGCCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTGCTTCTTACCCTGCC
CCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCCGTGCAAAAGCTACTTCCCCTACCTGA
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAG
ATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGGCTGCGGAACCGGAGC
CAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAAATCCCCACTTTGAGA
AGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGGCTCCT
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTG
CTCTGTGCAGAGCCCAAGGAAGTCTGCAGGAGTCCGGAGAGTACTGAGACCGGGAGGTGTGC
TCTTTTCTGGGAGCATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTC
GAGCCACCTGGAAACACATTGGGGATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGA
GAACGCCCAGTTCTCCGAAATCCAAATGGAACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTG
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCTCCAAGGCACTCATTGTCTCC
TTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTTA
GCAGAATGAGAGAAGACATTCATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG
AAACACTAGGACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTC
CCAATGTTGTCCCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACAC
CCATGCGTCTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGAC
CCTCTCTCCCCACTACCACCTTCTTCCTGAGCTGGGGGCACCAGGGAGAATCAGAGATGCTGGGG
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATATTTTTTAATAAATAGACGAA
ACCACG

FIGURE 28

MDILVPLLQLLVLLLTLP LHL MALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELF S QIKGL
TGASGKVALLELGCGTGANFQFYPPGCRVTC LDPNPHFEKFLT KSMAENRHLQYERFVVAPGEDM
RQLADGSMDVVVCTLVLC SVQSPRKVLQEVRRVLRPGGVLF FWEHVAEPYGSWAEMWQQVF EPTW
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWL PVGPHIMGKAVKQSF PSSKALICSFPSL
QLEQATHQPIYLP LRG T

Important features:

Signal peptide:

amino acids 1-23

Leucine zipper pattern.

amino acids 10-32

N-myristoylation sites.

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

FIGURE 29

CAATGTTTGCTATCCACCTCCCCAAGCCCCTTACCTATGCTGCTGCTAACGCTGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCTCTTCTG
CCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGCTCCTGCCTCAT
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGTGGGGGATGGCTTA
AGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGGGCTGCCTTATTTAAA
GTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGCCCTGTTTCATTAAGAAATT
GTTCCCTTCCCCTGTGTTCAATGTTTGTAAAGATTGTTCTGTGTAAATATGTCTTTATAATAAAC
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MLLLTLLLLLLLLLKGSCLWGLVGAQKVSSATDAFIRDWAFFPPSFLCLLPHRPAMTCSQAQPRG
EGEKVGDG

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

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FIGURE 31

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTT
CCTCCAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT
ATTTGCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATCTAAGTGAATCATGTCGG
GAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCCATGATGTTTACC
TTCAGATTCAACACACCTTCTGGTTCACATTTTCATTTTATTGTTTATTTGGGATTGTTGTT
TGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTGCTATCGTATCCACAGGCATCACGGCAGTG
CTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCAC
AAATAAAGCCATCAGCAGTCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCA
TTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTGAGCCTGGGAACGCAGGAGCTGCCAGGTT
ATGGAAGGCGCCAAGTGAATATAAGCCCCCTTCGGGCATTCGGTACATGTGGTCGTACCATTT
AATTGGCCTCATCTGGACTAGTGAATTCATCCTTGCGTGCCAGCAAATGACTATAGCTGGGGCAG
TGGTTACTTGTATTTCACAGAAGTAAAAATGATCCTCTGATCATCCCATCTTTTCGTCTCTC
TCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAG
GATTCCGAGAATCATTTGTATGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTC
AACCAGAATGCATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGC
ATTCAAAATCTTGTCCAAGAACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAA
TTTTTCTAGAAAGGTGTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTAC
AATCGGGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGC
CCATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGATC
TGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTTCGTA
AAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGA
GGGAACAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATT
TCCTTCTAAGAGCCATTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTT
TTAAAAGACCTAATAAACCTATTCTTCCTCAAAA

FIGURE 32

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIE
LDTERENMKCVLGFAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPFLFQPLWTF
ILIFFWVLWVAVLLSLGTAGAAQVMGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIA
GAVVTCYFNRSKNPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG
ALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD
FIIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLVAFFAYLVVHSLVSVFETVLDALFLCFA
VDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQDKHSLRNEEGTELQAIVR

Important features:

Signal peptide:

amino acids 1-20

Putative transmembrane domains:

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

N-glycosylation sites.

amino acids 204-208, 295-299, 313-317

N-myristoylation sites.

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

FIGURE 33

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGGACCTCTCCCTGTTTCTTCCTTAGA
 ATAATTTGTATGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCATTCTGTGTGGT
 GAAAATTTTTTGAAAAAAAATTCCTTCTTCAAACAAGGGTGTCTATCTGATATTTATGAGGAC
 TGTGTGTCTCCTATGAAAGCATCTGTTATTGAAATGTTCTTGTGTTTGTGCTGGTGAAGTAC
 ATTCAAACAAAGAAACGGCAAAGAAGATTAAAGGCCCAAGTTCAGTGTGCTCAGATCAACTGC
 GATGTCAAAGCCGAAAGATCATCGATCCTGAGTTCATTGTGAAATGTCCAGCAGGATGCCAAGA
 CCCCCAATACCATGTTTATGGCAGTACGTGTATGCATCCTACTCCAGTGTGTGTGGCGCTGCCG
 TACACAGTGGTGTGCTTGATAATTCAGGAGGGAAAATACTTGTTCGGAAGGTTGCTGGACAGTCT
 GGTACAAAGGGAGTTATTCACCGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTT
 TATCGTCTTAGAAAGTAAACCCAAAAAGGGTGAACCTACCCATCAGCTCTTACATACTCATCAT
 CGAAAAGTCCAGCTGCCCAAGCAGGTGAGACCACAAAAGCCTATCAGAGGCCACCTATTCAGGG
 ACAACTGCACAGCCGGTCACTCTGATGCAGCTTCTGGCTGTCACTGTAGCTGTGGCCACCCCCAC
 CACCTTGCCAAGGCCATCCCTTCTGCTGCTTCTACCACAGCATCCCAGACCACAATCAGTGG
 GCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCC
 AGAGCTGATCCAGGTATCCAAAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGC
 GGATGTCAGCCTGGGACTGTTCCTCAAAGAAGAATTGAGCACACAGTCTTTGGAGCCAGTATCCC
 TGGGAGATCCAACTGCAAAATGACTTGTCTGTTTTTAATTGATGGGAGCACCAGCATTGGCAAA
 CGGCGATTCCGAATCCAGAAGCAGCTCCTGGCTGATGTTGCCAAGCTCTTGACATTGGCCCTGC
 CGGTCCACTGATGGGTGTTGTCCAGTATGGAGACAACCTGCTACTCACTTTAACTCAAGACAC
 ACACGAATTCCTCGAGATCTGAAGACAGCCATAGAGAAAATTACTCAGAGAGGAGGACTTTCTAAT
 GTAGTCCGGGCCATCTCCTTGTGACCAAGAACTTCTTTCCAAAGCCAATGGAACAGAAGCGG
 GGATGCCCAATGTGGTGGTGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGCTTCAA
 GACTTGCGAGAGAGTCAAGGAATCAACATTTCTTTCATCACCATTGAAGGTGCTGCTGAAAATGAG
 AAGCAGTATGTGGTGGAGCCCACTTGCACAAAGGCCGTGTGCAGAACAAACGGCTTCTACTC
 GCTCCACGTGCAGAGCTGGTTTGGCTCCACAAGACCCTGCAGCCTCTGGTGAAGCGGGTCTGCG
 AACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAACCTGGCTGACATTGGCTTCGTCATCGAC
 GGCTCCAGCAGTGTGGGACGGGCACTTCCGCACCGTCTCCAGTTGTGACCAACCTCACCAA
 AGAGTTTGAGATTTCCGACACGGACACGCGCATCGGGGCCGTGCAGTACACCTACGAACAGCGGC
 TGGAGTTTGGGTTCCGACAAGTACAGCAGCAAGCCTGACATCCTCAACGCCATCAAGAGGGTGGGC
 TACTGGAGTGGTGGCACCAGCACGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
 GTCCAAAGCCCAACAAGAGGAAGTTAATGATCCTCATCACCAGCGGAGGTCTTACGACGACGTCC
 GGATCCCAGCCATGGCTGCCCATCTGAAGGGAGTGATCACCATATGCGATAGGCGTTGCCTGGGCT
 GCCCAAGAGGAGCTAGAAGTCAATGGCCACTCACCCGCCAGAGACCACTCCTTCTTGTGGACGA
 GTTTGACAACCTCCATCAGTATGTCCCCAGGATCATCCAGAACATTTGTACAGAGTTCAACTCAC
 AGCCTCGGAACTGAATTTCAGAGCAGGCAGAGCACCAGCAAGTGTCTTACTAACTGACGTGTT
 GGACCACCCACCGCTTAATGGGGCACGCACGGTGCATCAAGTCTTGGGCAGGGCATGGAGAAAC
 AAATGTCTTGTATTATCTTTGCCATCATGCTTTTTCATATTCCAAAACCTGGAGTTACAAAGA
 TGATCACAACGTATAGAATGAGCCAAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACAT
 TTTGACAATTGTTTTCAAATAAATGTTGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAG
 AGCTTTTGTGAGATTTTAAAGTTGTTATTTCTGATTTGAACTCTGTAACCTCAGCAAGTTTCAT
 TTTTGTGATGACAAATGTAGGAATGTGTAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAA
 AA
 AAG

FIGURE 34

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG
CQDPKYHVYGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWR
ESFIVLESKPKKGVTPSALTYSSSKSPAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA
TPTTLPRPSPAASTTSIPRPQSVGHRSEQMDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKP
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI
GPAGPLMGVVQYGDNPATHEFNKTHNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN
RSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG
FYSLHVQSWFGLHKTLPVLRVCDTDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN
LTKEFEISDTRIGAVQYTYEQRLFEGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQL
FKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQEELEVIATHPARDHSFF
VDEFDNLHQYVPRIIQNICTEFNSQPRN

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 181-200

N-glycosylation sites.

amino acids 390-394, 520-524

N-myristoylation sites.

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

Amidation site.

amino acids 304-308

[illegible]

APP ID=10063712

FIGURE 36

MASALWTVLPSRMSLRSLKWSLLLLLSLFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQDFHF
TLREHSNCSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLA
LSLEDEHLLYGDIIRQDFLDTYNNLTlKTIAMFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLl
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQYEPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV
KPIKFEDVYVGICLNLKVNlHIPEDTNLFFLYRIHLDVQQLRRVIAAHGFSSKEIITFWQVMLR
NTTCHY

Important features:

Type II transmembrane domain:

amino acids 20-39

N-glycosylation sites.

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

Glycosaminoglycan attachment site.

amino acids 239-243

Ly-6 / u-PAR domain proteins.

amino acids 23-37

N-myristoylation site.

amino acids 271-277

FIGURE 37

CGCTCGGGCACAGCCGCGGCAAGGATGGAGCTGGGTGCTGGACGAGTTGGGGCTCACTTTCTTCAGCTCCTTCATC
TCGTCTTGGCAAGAGAGTACACAGTCATTAATGAAGCTGCCCTGGAGCAGAGTGGAAATATCATGTGTCGGGAGTGCTGTG
AATATGATCAGATTGAGTGCGTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCCTTGCTGCAGGAATGAGGAGAA
TGAGTGTGACTCCTGCCGTATCCACCCAGGTTGTACCATCTTTGAAAACGCAAGAGCTGCCGAAATGGCTCATGGGGGGGT
ACCTTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCCATGTG
GCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTGTGGAAGCTATCCCTTAAATGCTCACGTGTAATGGACCATTATGTC
TAAACCTGGGTTTGTCTCACTCACTAAGATTGTCTATGTTGAGTCTGGAGTTTACTACATGTGCCAGTATGACTATGTTGAG
GTTCTGTATGGAGACAACCGCATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCATCCAGAGCATAG
GATCCTCACTCCACGCTCTCTTCCACTCCGATGGCTCCAAGAAATTTGACGGTTTCCATGCCATTATGAGGAGATCACAGC
ATGCTCCTCATCCCTTGTTCATGACGGCACGTGCGTCTTGACAAGGCTGGATCTTACAAGTGTGCTGCTTGGCAGGC
TATACTGGGCGCGCTGTGAAATCTCCCTTGAAGAAAGAACTGCTCAGACCCTGGGGGCCAGTCAATGGGTACCAAGAAA
TAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGTCTAAAATTGGCACCCTGGTGTCTTCTTTTGTAACTCTTATGT
TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGTGGTCAAGGAAACAGCCCATCTGCATAAAGCCTGCCGA
GAACCAAGATTTTCAGACC TGGTGAGAGGAGAGTTCTTCCGATGCAGGTTCAAGGAGACACCATTACACCAGCTAT
ACTCAGCGGCCCTTCAGCAAGCAGAACTGCAGAGTGCCCTACCAAGAGCCAGCCCTTCCCTTTGGAGATCGCCCATGGG
ATACCAACATCTGCATACCCAGTCCAGTATGAGTGCACTTCACCTTCTACCGCCGCTGGGCGAGCAGGAGGACATGT
CTGAGGAGTGGGAAGTGGAGTGGCGGGCCACCATCTGCATCCCTATCTGCGGGAAAATTGAGAACATCACTGCTCCAAAGA
CCCAAGGTTGCGCTGGCGTGGCAGGCAGCCATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCCTACACAAGGGAGC
GTGTTCTTACTGTGACGCGGTGCCCTGGTGAATGAGCGCACTGTGTTGGTGGCTGCCCATGTGTTACTGACCTGGGGAAG
GTCAACATGATCAAGACAGCAGACCTGAAAGTTGTTTGGGGAAATCTACCGGGATGATGACCGGGATGAGAAGACCATCC
AGAGCCTACAGATTTCTGCTATCATCTGCACTCCAACTATGACCCATCTGCTTGATGCTGACATCGCCATCTGAAAGCT
CCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCCTGCTGCGCAGTCCGGATCTCAGCACTTCTTCCAGGAG
TCCACATCACTGTGGCTGGCTGGAATGCTTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGG
TGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGAGTGTACATGATAACATGTT
CTGTGCCAGCTGGGAACCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGGCATCGCGCTGTGTTCTCCGGGA
CGAGCATCTCCTGAGCCACGCTGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGACGCCACAGGCTCTCCA
CTGCCCTTCAACCAAGGTCTGCCCTTTTAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAG
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACCTGGCT
GTGCCAGGGCTTCTGACTTCAGGGACAAAACCTCAGTGAAGGGTGAAGTAGACCTCCATTGCTGGTAGGCTGATGCCGCTCCA
CTACTAGGACAGCAATTGGAAGATGCCAGGGCTTGAAGAAGTAAGTTCTTCAAGAAGACCATATACAAAACCTCTCCA
CTCCACTGACCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAG
GCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCCTT
TGTGTACATGGCCACAGTACAGTCTGGTCTTTTCTTCCCATCTCTTGTACACATTTTAAATAAAATAAGGGTTGGCTTCT
GAACTACAAAAA
AAAAA

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII
KRVCGNERPAPIQSIGSSSLHVLFSHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDFGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFQKQLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
KTQGLRWPAQAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL
KVVLGKFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASR
DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLFPKDWI
ERNMK

Important features of the protein:

Signal peptide:

amino acids 1-23

EGF-like domain cysteine pattern signature.

amino acids 260-272

N-glycosylation sites.

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
474-480, 491-497, 638-644, 666-672

Amidation site.

amino acids 56-60

Serine proteases, trypsin family.

amino acids 489-506

CUB domain proteins profile.

amino acids 150-167

FIGURE 39

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAAACGTGGCTTAATC
 TGAAGGTTCTCAGTCAAATTCCTTGTGATCTACTGATTGTGGGGCATGGCAAGGTTTGCTTAAAGGAGCTTGGCTGG
 TTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGSAGAATGAAGGCGCTTCTGTTGC
 TGGTCTTGCCCTTGCTCAGTCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCGTATTGAGAACTCTGTA
 AAGGTGCCTCCCACTACGGCCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAGACGGCTGTGCGAGCC
 TCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAGACGAGCCTGGCCTAGACA
 ACCCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCAGTGGACTCTGGCCGGAGCAACCGAACTA
 GGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAAATCGAGCTTTGAGTGTTCTTCGAA
 GGACAAAGAGCGGGAGTGCAGTTGCCAACCATGCCAGCAGGGCAGGGAATTTCTGAAAACACCACTGCCCTGAAG
 TCTTTCCAAGTTGTACCACTGATTCCAGATGGTGAAATACCAGCATCAAGATCAATCGAGTAGATCCCACTGAAA
 GCCTCTCTATTAGGCTGGTGGGAGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTATCGTGATGGGG
 TGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTCTAAAGGTCAACGGGATGGACATCAGCAATGCTCCCTC
 ACAACTACGCTGTGCGTCTCCTGCGGAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCA
 GCAGGAACAATGGACAGGCCCGGATGCCACAGACCCCGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCC
 CCGAGGAGCAGCTTGAATAAACTGGTGCAGCAAGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCG
 GTGTGGCATATCGACATGGTCACTTGGAGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCA
 GCCCAGAAAGTGCGGCTCATCTGATTGAGGCCAGTGAAGACGTGTTACCTCGTCTGTCCCGCAGGTTGCGCAGC
 GGAGCCCTGACATCTTTCAGGAAGCCGGTGGAAACAGCAATGGCAGTGGTCCCAGGGCCAGGGAGAGGAGCAACA
 CTCCCAAGCCCTCCATCCTACAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAGACCCCGGTGAATCTCTCG
 GCATGACCGTGCAGGGGGAGCATCACATAGAGAATGGGATTGCTTATCTATGTGATCAGTGTGAGCCCGAGGAG
 TCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTGTTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCC
 GGAGTGAGGCAGTGGCATTATTGAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGC
 CCCAGGAAGACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTCACTGGTCCCCATCCT
 GGGTCATGTGGCTGGAATTACCACGGTCTTGTATACTGTAAGATATTGTATTACGAAGAAACACAGCTGGAAGTC
 TGGGCTTCTGCATTGTAGGAGTTATGAAGAATACAATGGAAACAAACCTTTTTTCATCAATCCATTGTTGAAGGAA
 CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGTCTCAATGGTAGAAGTACATCAGGAATGA
 TACATGCTTGCTTGGCAAGACTGCTGAAAGAATTAAGGAAGAATTAATCTAACTATTGTTTCTTGGCCTGGCACTT
 TTTTATAGAATCAATGATGGGTGAGAGGAAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACTATATTATC
 TTGTGATTTTTATATTTAAAGAAAGATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAATGAAAGCCAGTT
 ACACCTCAGAAAAATGATTCAAAAAATTAATACTACTAGTTTTTTTTCAGTGTGGAGGATTCTCATTACTCTAC
 AACATTGTTTATATTTTTCTATTAATAAAAGCCCTAAAACAATAAATGATTGATTTGTATACCCCACTGAATT
 CAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTAAATTTACAGCT
 AAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAACAAGAATAAATATTTTTTCAGAAGTTAAA

FIGURE 40

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRSQDGCPCDGCASLTATAPS
PEVSAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSEFKKINR
ALSVLRRTKSGSAVANHADQGRESENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV
GGSETPLVHIIIIQHIYRDGVIARDGRLLPGDIILKVNCGMDISNVPHNYAVRLLRQPCQVLWLTVM
REQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGVFIENVLDGGVAYRHG
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVQRSPDIFQEAGWNSNGSWSPG
PGRSNTPKPLHPTITCHEKVNIQKDPGESLGMTVAGGASHREWDLPYVISVEPGGVISRDGR
IKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP
SDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFPIKSIVEGTPAYNDG
RIRCGDILLAVNGRSTSGMIHACLARLLKELKGRITLTIVSWPGTFL

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-112, 157-161, 289-293, 384-388

Tyrosine kinase phosphorylation sites.

amino acids 433-441, 492-500

N-myristoylation sites.

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,
467-473, 603-609

APP ID=10063712

FIGURE 41

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTT
CTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACT
TTCCACCTTTCCCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGTGGGC
CACCAGTAACTACTTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTTCC
ATAAGACCTCATTTTGGGAAGGGAAAACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAATT
GACAACTGTCCTTCTGTGTCCTTACCTCAGAGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCAC
TTTGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAG
CTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAA
CATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGG
TAAAAAGTTAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG
ACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAG
CATCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTG
GGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACTACTGGGGAT
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTG
CCTGAAGTGGGTAAATATACAATGGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG
GATGAAGCTCTTACACCAAGTGTACGAGTCTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAT
TAGTATCTGTGGAACACAATCCTTTATATATCAACATCAGTGGATTTCTGGTTTGGTGCATGACCC
TGGATCTTTTGGTGATGTTTGAAGAAGTATTCTTTGTTTGCAATAATTTTGGCCTAGAGACTTCAA
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTTCCTTTTGTATTTCT
TAGCAGAGCTCCTGGTGATGTAGAGTATAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGAT
CATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGATAA
AATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATATTATGGGAT
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAA
AGGTACGAAGATACAATACTGTTATTTCATTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGT
GAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGA
GGTAGCAGGAGGGTGGAGTGTGGCTGCAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC
CTTCAGGGGAGGACCTGCCAGGTATGCCTTCCAGTGATGCCACCAGAGAATACATTCTCTATTAGT
TTTTAAAGAGTTTTTGTAAAATGATTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACAT
ATTAACATAATAAATATGTCTATCAAATACCTCTGTAGTAAAATGTGAAAAAGCAAAA

FIGURE 42

MGFNLT FHL SYKFRLLLLLTCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTN
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH
RNREKHLMYLLEHLHPFLQRQQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFI FHDV
DLVPENDFNLYKCEEHPKHLVGRNSTGYRLRYSGYFGGV TALSREQFFKVNGFSNNYWG WGGED
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV
SVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

APP ID=10063712

Year	Country	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)
1950	United States	150.7	80.0	53.1	26.0	100.0
1955	United States	157.3	85.0	54.1	27.0	100.0
1960	United States	162.9	90.0	55.3	28.0	100.0
1965	United States	169.1	95.0	56.2	29.0	100.0
1970	United States	175.3	100.0	57.1	30.0	100.0
1975	United States	181.5	105.0	58.0	31.0	100.0
1980	United States	187.7	110.0	58.9	32.0	100.0
1985	United States	193.9	115.0	59.3	33.0	100.0
1990	United States	200.1	120.0	60.0	34.0	100.0
1995	United States	206.3	125.0	60.6	35.0	100.0
2000	United States	212.5	130.0	61.2	36.0	100.0
2005	United States	218.7	135.0	61.8	37.0	100.0
2010	United States	224.9	140.0	62.3	38.0	100.0
2015	United States	231.1	145.0	62.9	39.0	100.0
2020	United States	237.3	150.0	63.4	40.0	100.0
2025	United States	243.5	155.0	63.7	41.0	100.0
2030	United States	249.7	160.0	64.3	42.0	100.0
2035	United States	255.9	165.0	64.5	43.0	100.0
2040	United States	262.1	170.0	64.9	44.0	100.0
2045	United States	268.3	175.0	65.2	45.0	100.0
2050	United States	274.5	180.0	65.6	46.0	100.0
2055	United States	280.7	185.0	66.0	47.0	100.0
2060	United States	286.9	190.0	66.4	48.0	100.0
2065	United States	293.1	195.0	66.7	49.0	100.0
2070	United States	299.3	200.0	67.0	50.0	100.0
2075	United States	305.5	205.0	67.3	51.0	100.0
2080	United States	311.7	210.0	67.5	52.0	100.0
2085	United States	317.9	215.0	67.8	53.0	100.0
2090	United States	324.1	220.0	68.0	54.0	100.0
2095	United States	330.3	225.0	68.3	55.0	100.0
2100	United States	336.5	230.0	68.5	56.0	100.0
2000	China	1,212.0	310.0	25.6	152.0	39.0
2005	China	1,268.0	320.0	25.3	158.0	40.0
2010	China	1,324.0	330.0	25.0	164.0	41.0
2015	China	1,380.0	340.0	24.6	170.0	42.0
2020	China	1,436.0	350.0	24.4	176.0	43.0
2025	China	1,492.0	360.0	24.1	182.0	44.0
2030	China	1,548.0	370.0	23.9	188.0	45.0
2035	China	1,604.0	380.0	23.7	194.0	46.0
2040	China	1,660.0	390.0	23.5	200.0	47.0
2045	China	1,716.0	400.0	23.3	206.0	48.0
2050	China	1,772.0	410.0	23.1	212.0	49.0
2055	China	1,828.0	420.0	23.0	218.0	50.0
2060	China	1,884.0	430.0	22.8	224.0	51.0
2065	China	1,940.0	440.0	22.7	230.0	52.0
2070	China	1,996.0	450.0	22.6	236.0	53.0
2075	China	2,052.0	460.0	22.4	242.0	54.0
2080	China	2,108.0	470.0	22.3	248.0	55.0
2085	China	2,164.0	480.0	22.2	254.0	56.0
2090	China	2,220.0	490.0	22.1	260.0	57.0
2095	China	2,276.0	500.0	22.0	266.0	58.0
2100</						

Year	Country	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)
1950	United States	150.7	80.0	53.1	26.0	100.0
1955	United States	157.3	85.0	54.1	27.0	100.0
1960	United States	162.9	90.0	55.3	28.0	100.0
1965	United States	169.1	95.0	56.2	29.0	100.0
1970	United States	175.3	100.0	57.1	30.0	100.0
1975	United States	181.5	105.0	58.0	31.0	100.0
1980	United States	187.7	110.0	58.9	32.0	100.0
1985	United States	193.9	115.0	59.3	33.0	100.0
1990	United States	200.1	120.0	60.0	34.0	100.0
1995	United States	206.3	125.0	60.6	35.0	100.0
2000	United States	212.5	130.0	61.2	36.0	100.0
2005	United States	218.7	135.0	61.8	37.0	100.0
2010	United States	224.9	140.0	62.3	38.0	100.0
2015	United States	231.1	145.0	62.9	39.0	100.0
2020	United States	237.3	150.0	63.4	40.0	100.0
2025	United States	243.5	155.0	63.7	41.0	100.0
2030	United States	249.7	160.0	64.3	42.0	100.0
2035	United States	255.9	165.0	64.5	43.0	100.0
2040	United States	262.1	170.0	64.9	44.0	100.0
2045	United States	268.3	175.0	65.2	45.0	100.0
2050	United States	274.5	180.0	65.6	46.0	100.0
2055	United States	280.7	185.0	66.0	47.0	100.0
2060	United States	286.9	190.0	66.4	48.0	100.0
2065	United States	293.1	195.0	66.7	49.0	100.0
2070	United States	299.3	200.0	67.0	50.0	100.0
2075	United States	305.5	205.0	67.3	51.0	100.0
2080	United States	311.7	210.0	67.5	52.0	100.0
2085	United States	317.9	215.0	67.8	53.0	100.0
2090	United States	324.1	220.0	68.0	54.0	100.0
2095	United States	330.3	225.0	68.3	55.0	100.0
2100	United States	336.5	230.0	68.5	56.0	100.0
2000	China	1,212.0	310.0	25.6	150.0	39.0
2005	China	1,268.0	320.0	25.3	155.0	40.0
2010	China	1,324.0	330.0	25.0	160.0	41.0
2015	China	1,380.0	340.0	24.6	165.0	42.0
2020	China	1,436.0	350.0	24.4	170.0	43.0
2025	China	1,492.0	360.0	24.1	175.0	44.0
2030	China	1,548.0	370.0	23.9	180.0	45.0
2035	China	1,604.0	380.0	23.7	185.0	46.0
2040	China	1,660.0	390.0	23.5	190.0	47.0
2045	China	1,716.0	400.0	23.3	195.0	48.0
2050	China	1,772.0	410.0	23.1	200.0	49.0
2055	China	1,828.0	420.0	23.0	205.0	50.0
2060	China	1,884.0	430.0	22.8	210.0	51.0
2065	China	1,940.0	440.0	22.7	215.0	52.0
2070	China	1,996.0	450.0	22.6	220.0	53.0
2075	China	2,052.0	460.0	22.4	225.0	54.0
2080	China	2,108.0	470.0	22.3	230.0	55.0
2085	China	2,164.0	480.0	22.2	235.0	56.0
2090	China	2,220.0	490.0	22.1	240.0	57.0
2095	China	2,276.0	500.0	22.0	245.0	58.0
2100</						

FIGURE 44

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPI
CIFCCGCCHRSKCGMCCKT

Important features:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 58-59

N-myristoylation site.

amino acids 44-50

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 1-12

APP ID=10063712

FIGURE 45

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC
TCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT
TCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTG
GACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAG
AAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCA
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCA
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATT
TATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC
CTGGAGATGGGGAGAACTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACT
TCTCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATG
GTCTCTCTGTGTCTCCTGTTGGTGGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTG
GTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCGGG
AAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT
AGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCAGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTA
TCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 46

MAGSPTCLTLIIYLWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQP
EGGTIIIVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSK
PKVTMGLQSNKNGTCVTNLTCMEHGEEVDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIC
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIE
EKKRVDICRETPNICPHSGENTYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT
PRLFAYENVI

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 224-250

Leucine zipper pattern.

amino acids 229-251

N-glycosylation sites.

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,
291-295

FIGURE 47

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCAATGACCTGCTGCGAAGGATGGACATCCTGCAATGG
ATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCT
TAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATT
ATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG
CTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCACAGTCATTGGTGCTC
TGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATGTGTAATTCTCCAAGC
AACAGTAATGCCAATTGTGAATTTTCATTGAAAACATCAGTGACATTCATCCAGAATCCTTCAA
CTTGCACTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCACCAGTAACG
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGG
CTTATCCACTTCTCAGTATTTTAGGTCTATTGCTTGTTGGAATTCCTGGAGGTCCTGTTTGGGCT
CAGTCAGATAGTCATCGGTTTCCTTGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTG
TGTAGTTTAATGGGAATAAAATGTAAGTATCAGTAGTTTGAAAAAAAAA

FIGURE 48

MTCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA
TTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCLISIQALLKGPLMCNSPSNSNANCEFSL
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDFSEENKHLIHFSVFLGL
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

Important features:

Transmembrane domains:

amino acids 10-31 (type II), 50-72, 87-110, 191-213

N-glycosylation sites.

amino acids 80-84, 132-136, 148-152, 163-167

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 223-227

N-myristoylation sites.

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 207-218

TNFR/NGFR family cysteine-rich region protein.

amino acids 4-12

FIGURE 49

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGA
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGA
CATGGGAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACC
CATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC
TGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAAATGCAAATACAAGAG
CAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA
CTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACC
TCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCAAGGGCAGGCTGTTAGGCCCCCT
TTCTGATCAGGAGGCTTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

FIGURE 50

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS
SQKQHSFPVPEKAIPPLITPGSATTC

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 36-59

N-myristoylation sites.

amino acids 41-47, 45-51, 84-90

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.

amino acids 54-67

FIGURE 51

GTGGA CTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG
AGGACAGGGAGT CGGAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCGGCCAAGG
AGGAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGGCAGAGATGAAGTTCCAG
GGGCCCCCTGGCCTGCCTCCTGCTGGCCCTCTGCCTGGGCAGTGGGGAGGCTGGCCCCCTGCAGAG
CGGAGAGGAAAGCACTGGGACAAATATTGGGGAGGCCCTTGGACATGGCCTGGGAGACGCCCTGA
GCCAAGGGGTGGGAAAGGCCATTGGCAAAGAGGCCGGAGGGGCAGCTGGCTCTAAAGTCAGTGAG
GCCCTTGGCCAAGGGACCAGAGAAGCAGTTGGCACTGGAGTCAGGCAGGTTCCAGGCTTTGGCGC
AGCAGATGCTTTGGGCAACAGGGTCGGGGAAGCAGCCCATGCTCTGGGAAACACTGGGCACGAGA
TTGGCAGACAGGCAGAAGATGTCATTCGACACGGAGCAGATGCTGTCCGCGGCTCCTGGCAGGGG
GTGCCTGGCCACAGTGGTGCTTGGGAAACTTCTGGAGGCCATGGCATCTTTGGCTCTCAAGGTGG
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGACTCCGTGGGTCCACGGATACCCCG
GAAACTCAGCAGGCAGCTTTGGAATGAATCCTCAGGGAGCTCCCTGGGGTCAAGGAGGCAATGGA
GGGCCACCAAACCTTTGGGACCAACACTCAGGGAGCTGTGGCCAGCCTGGCTATGGTTCAGTGAG
AGCCAGCAACCAGAAATGAAGGGTGACGAATCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA
ACTCTGGGGGAGGCAGCGGCTCACAGTCGGGCAGCAGTGGCAGTGGCAGCAATGGTGACAACAAC
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAG
TGGCGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGT
CCTCCTGGGGATCCAGCACCGGCTCCTCCTCCGGCAACCACGGTGGGAGCGGCGGAGGAAATGGA
CATAAACCCGGGTGTGAAAAGCCAGGGAATGAAGCCCGGGAGCGGGGAATCTGGGATTCAGGG
CTTCAGAGGACAGGGAGTTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATCGCCTCCTTG
GAGGCTCTGGAGACAATTATCGGGGGCAAGGTCGAGCTGGGGCAGTGGAGGAGGTGACGCTGTT
GGTGGAGTCAATACTGTGAACCTCTGAGACGTCTCCTGGGATGTTTAACCTTTGACACTTTCTGGAA
GAATTTTAAATCCAAGCTGGGTTCATCAACTGGGATGCCATAAACAAGGACCAGAGAAGCTCTC
GCATCCCGTGACCTCCAGACAAGGAGCCACCAGATTGGATGGGAGCCCCACACTCCCTCCTTAA
AACACCACCTCTCATCTAATCTCAGCCCTTGCCCTTGAAATAAACCTTAGCTGCCCCACAAA
AA
AA

FIGURE 52

MKFQGPLACLLLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIKEAGGAAGSKVS
EALQQTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVF
GHSGAWETSGGHGIFGSQGGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWQGGNGGPPNF
GTNTQGAQAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGGS
SSGSSSGSSSGSGSGSGSSSGSSGSGSRGDSGSESSWGSSTGSSSGNHGGS GGGNGHKPGCEKPGNE
ARGSGESGIQGFRRQGVSSNMREISKEGNRLGSGSDNYRGQSSWGS GGGDAVGGVNTVNSETPGM
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

[illegible][illegible]

FIGURE 54

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPPKRNWFWGHLG
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP
WLGEGILLSGGDKWSRHRMLTPAFHFNIILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC
RLVHDFTDVIRERRRTLPQTQIDDDFFKDKAKSKTLDLDFIDVLLLSKDEDEGKALSDEDIRAEADTF
MFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDFRFDPENSKGRSP
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN
VGLQ

Important features:

Transmembrane domains:

amino acids 13-32 (type II), 77-102

Cytochrome P450 cysteine heme-iron ligand signature.

amino acids 461-471

N-glycosylation sites.

amino acids 112-116, 168-172

FIGURE 55

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTTGA
GCCTACTCGTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACTTACCCTGTGTTCTGCCT
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTTGGCATTGACGTGG
TACAGCCTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTGCTTGC
ATAATTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAGCTGGTGGACAGTTTT
GTAACATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCTTGCAGCAATGTGTTGCTT
GTGATTGGAACATTTGAGGGTTACTTTTGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA
GCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGGAACTTCCTCATGTACCTGTTTCCTC
TCTGGATGTTGTCCCACTGAATTCCCATGAATACAAACCTATTGAGCAACAGCAAAAAAAAAAAAA
AA

FIGURE 56

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFAR
DAVKKCFVCLA

Important features:

Signal peptide:

amino acids 1-33

Type II fibronectin collagen-binding domain protein.

amino acids 30-72

FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACATGCTCTGTCTGTGCCTG
TACGTGCCGGTCATCGGGGAAGCCAGACCGAGTTCAGTACTTTGAGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCC
ATTTTCAAGCTCAGTGTCTTCATCCCTCCAGGAATTCTCCACCTACCGCCAGTGGGAAGCAGAAAAATTGTACAAGCT
GGAGATAAGGACCTTGATGGGCAGCTAGACTTTGAAGAATTGTCCATTATCTCCAAGATCATGAGAAGAGCTGAGG
CTGGTGTTTAAGATTTTGGACAAAAAGATGATGGACGCATTGACGCCGAGGAGATCATGCAGTCCCTGCGGGGACTTG
GGAGTCAAGATATCTGAACAGCAGGCCAGAAAAATTCTCAAGAGCATGGATAAAACGGCACGATGACCATCGACTGG
AACGAGTGGAGAGACTACCACCTCCTCCACCCGTGGAAAAATCCTCCGAGATCATCTCTACTGGAAGCATTTCCACG
ATCTTTGATGTGGGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCAGACGGGGATGTGGTGAGA
CACCTGGTGGCAGGAGGTGGGGCAGGGCCGTATCCAGAACCTGCACGCCCCCTGGACAGGCTCAAGGTGCTCATG
CAGGTCATGCTCCCGCAGCAACAATGGGCATCGTTGGTGGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGG
TCACTTGGCGGGCAATGGCATCAACGTCTCAAAATTGCCCCGAATCAGCCATCAAAATCATGGCCTATGAGCAG
ATCAAGCGCCTTGTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGCTCCTTGGCAGGGGCC
ATCGCCCAAGCAGCATCTACCAATGGAGGTCTGAAGACCCGGATGGCGCTGCGGAAGACAGGCCAGTACTCAGGA
ATGCTGGATGCGCCAGGAGGATCCTGGCCAGAGAGGGGTGGCCGCTTCTACAAAGGCTATGTCCCAACATGCTG
GGCATCATCCCTATGCCGGCATCGACCTTGCACTCTACGAGACGCTCAAGAATGCTGGCTGCAGCACTATGCAGT
AACAGCGCGGACCCCGGCTGTTTGTGCTCCTGGCTGTGGCACCATGTCCAGTACCTGTGGCAGCTGGCCAGCTAC
CCCTGGCCCTAGTCAGGACCCGGATGCAGCGCAAGCCTCTATTGAGGGCGCTCCGGAGGTGACCATGAGCAGCTC
TTCAACATATCTGCGGACCGAGGGGGCTTGGGGCTGTACAGGGGGCTGGCCCCAATTCATGAAGGTGATCCCA
GCTGTGAGCATCAGTACGTGGTCTACGAGAACCTGAAGATCACCTGGGGCTGCAGTCCGGGTGACGGGGGAGGGC
CGCCCCGAGTGGACTCGCTGATCCTGGCCGAGCCTGGGGTGTGCAGCCATCTCATTCTGTGAATGTGCCAACCT
AAGCTGTCTCGAGCCAGCTGTGAAACCTTAGACGCACCCGAGGAGGGTGGGGGAGAGCTGGCAGGCCAGGGCTT
GTCTGTGACCCAGCAGACCTCCTGTTGGTTCCAGCGAAGACACAGGCATTCCTTAGGGTCCAGGGTCAAGCAGG
CTCCGGGCTCAGATGTGTAAGGACAGGACATTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGGCT
TAGTTCTTCCATTTCAACCTTGCAGCCAGCTGTGGCCACGGCCCTGCCCCTCTGGTCTGCCGTGCATCTCCCTGTGC
CCTCTTGTGCTGCTGTCTGCTGAGGTAAGGTGGAGGAGGGCTACAGCCACATCCACCCCTCGTCCAATCCC
ATAATCCATGATGAAAGGTGAGGTACGTGGCTCCAGGCTGACTTCCCACTACAGCATTGACGCCAATTTGGC
TGTGAAGGAAGAGGAAGGATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTCGGGCATG
CTTGGGAGTGCAGGGGGCTCGGGCTGCTGGCTGGCTGCACAGAAGGCAAGTGTGGGGCTCATGGTGTCTGAGCT
GGCCTGGACCTCTCAGGATGGGCCCCACCTCAGAACCCTCACTGTCCCCACTGTGGCATGAGGGCAGTGGAGCA
CCATGTTTGAAGGGCAGGGCAGAGCGTTTGTGTGTTCTGGGGAGGGAAGGAAAGTGTGAGGGCTTAATTTATGG
ACTGTTGGGAAAAGGGTTTTGTCCAGAAGGACAGCCGGACAAATGAGCGACTTCTGTGCTTCCAGAGGAAGACGAGG
GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTCCAACCCAGCAGGGGCGCAGC
GGGACAGCCCCACATTCACCTTGTGTCACTGCTTGAACCTATTTATTTTGTATTTATTTGAACAGAGTTATGTCCT
AACTATTTTATAGATTTGTTAATTAATAGCTTGTCAATTTCAAGTTCAATTTTATTCATATTTATGTTTATGTT
GATTGTACCTTCCCAAGCCCGCCAGTGGGATGGGAGGAGGAGGAGGAGGAGGGGGGCTTGGGCCGCTGCAGTCACATCT
GTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAAGCGCCAGAGGCAGCAGCCCTGGCTCCTTTCTTTGGCAG
GTTGGGAAGGGCTTGCCCCAGCCTTAGGATTTAGGGTTTGAAGTGGGGCGTGGAGAGAGGGGAGGAACCTCAAT
AACCTTGAAGGTGGAATCCAGTTATTTCTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCAG
TGAGGTGCTCTCACTGTGAATTTTGGTGGGGGGGGCTGGAGGAGAGGGTGGGGGGCTGGCTCCGTCCTCCAGC
CTTCTGCTGCCCTTGTCTAACATGCCGGCACTGGCGACCTCACGTTGCACTTCCATTCACCAAGATGACCTGA
TGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAATTTGTATATATGAACATATAACTGGAGTCGTCAAAAG
CAATTAAGAAAGATTTGACGTTAGAAGTTGTCAATTTAAGCAGCCTTCAATAAAGTTGTTTCAAAGCTGAAAAA
AAA

FIGURE 58

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKDLDG
QLDFEEFVHYLQDHEKKLRLLVFKILDKKNDGRIDAQEI MQSLRDLGVKISEQQAEKILKSMDKNG
TMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTPDEFTVEERQTGMWWRHVAGGG
AGAVSRTCTAPLDRLKVL MQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIAK
FMAYEQIKRLVGSDQETLRIHERLVAGSLAGAI AQSSIYPMEVLKTRMALRKTGQYSGMLDCARR
ILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSTC
GQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYV
VYENLKITLGVQSR

Important features:

Signal peptide:

amino acids 1-16

Putative transmembrane domains:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation sites.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGC
 TTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG
 CACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCAGTCACTACTGTGCCTCAGCT
 GGGAAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAAACCTTCTGATAT
 CGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCAAAGAAGGCAAAGATG
 AGCTGTGGAGCAGGATGAAATGTTGAGGGCCGGACAGCAGTGTGTTGCTGATCAAGTGATAGTT
 GGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGTTATAT
 CATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGG
 AAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCC
 CAGCCCACAGTGGTCTGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATAC
 CAGCTTTGAGCTGAACTCTGAGAATGTGACCATGAAGTTGTGTCTGTGCTCTACAATGTTACGA
 TCAACAACACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTG
 ACAGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGT
 CTCTTCTTTCTTTGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATGCTAAAATAAT
 GTGCCTTGCCCAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
 CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG
 AGCAAACAAGAGCAAGAAACAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAAT
 CTATCTTCAAAGACATATTAGAAGTTGGGAAAATAATTCATGTGAAC TAGACAAGTGTGTTAAGA
 GTGATAAGTAAATGCACGTGGAGACAAGTGCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT
 CACCTGGGGAGTGAGAGGACAGGATAGTGATGTTCTTTGTCTCTGAATTTT TAGTTATATGTGC
 TGTAATGTTGCTCTGAGGAAGCCCCGAAAGTCTATCCCAACATATCCACATCTTATATTCCAC
 AAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGGGGCG
 GCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGCGCTTC
 TCTTCCCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGT
 CGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 60

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS
DIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKC
YIITSKKGKNANLEYKTGAFSMPEVNVNDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVS
NTSFELNSENVTMKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESIKRRLSHLQLLNSKASL
CVSSFFAISWALLPLSPYMLK

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 258-281

N-glycosylation sites.

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,
220-224

N-myristoylation sites.

amino acids 52-58, 126-132, 188-194

FIGURE 61

TGACGT CAGAAT CACCA ATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG
CACCAGGAGCCCCTCCGGGTAGCTACTACCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGT
GGGCTACCCCTGGTGGTGGTTATGGGGTCTGCCCCTGAGGGCCTTATGGACCACCAGCTGG
TGGAGGGCCCTATGGACACCCCAATCCTGGGATGTTCCCTCTGGAACCTCAGGAGGACCATATG
GCGGTGCAGCTCCCGGGGGCCCCATGGTGCAGCCACCTCCAAGTTCTACGGTGCCAGCAGCCT
GGGCTTTATGGACAGGGTGGCGCCCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTTCCAGTC
GGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA
ATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCA
GGCCGCATCGATGTCTACGGCTTCTCAGCCCTGTGGAATTCATCCAGCAGTGGGAAGACCTCTT
CCAGCAGTATGACCGGGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCC
AAATGGGCTACAACCTGAGCCCCAGTTACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCT
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA
GGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCTCAGCTTCGAGGACTTCGTCA
CCATGACAGCTTCTCGGATGCTAT TGACCCCAACCATCTGTGGAGAGTGGAGTGCACAGGGACCTT
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCTGCATCATAGCCACCA
AATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGA
ATGTCTGATGGCCATGAGCAGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAATGG
AGTTAGTGTCCAGTCAGCTGAGCTCCACCTGATGCCAGTGGTGGTGTTCATCGGCCTGTTACC
GTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAACGAGCCCATTTTCTCCAAAGTGGAAT
CTGACCAAGCATGAGAGAGATCTGTCTATGGGACAGTGGCTTGGATTCTGCCACACCCATAAAT
CCTTGTTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGGCAT
CTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCT
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTGCAATTTTTTTC
ATTTGGGGCCAAAAGTCCAGTGAAATGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 62

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYG
HPNPGMFPSGTPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSH
SGYISMKELKQALVNCNWSSFNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDR
DRSGSISYTELQQALSQMGYNLSPQFTQLLVSRYPERSANPAMQLDRFIQVCTQLQVLTEAFREK
DTAVQGNIRLSFEDEFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-
66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 63

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATC
TCCCAGGCCTCTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACC
AACTTGCCTCAGCTCGGACAACCTTCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGC
TCTGGACCCCTAGGTCTAATGACTTGGCAAGGGTTCTCTGAAGCTCAGCGTGCCTCCATCAGATG
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGGCTGCCTGCCATG
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACCGCCTGGGGGA
AGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGTGCGGCCCTCGCTCCGGGCAGTGGCCCTT
TGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGAC
TCGGAGTCCAGACGACTGCCCCGTTCTAATTCACTGGGAGCCGGGGGAAAAATCCTTTCCCAACG
CCCTCCCTGGTCTCTCATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTG
TGTCTGGGGAGGTGGAGGCCCTGGGACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGA
ATCTGGGGTATCAATAATCAACCCCCAGGTACCAGCTGGGGAAATATTAATCGGTATCCAGGAGG
CAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTAATCGGTATCCAGGAG
GCAGCTGGGGGAATATTATCTATACCCAGGTATCAATAACCCATTTCTCCTGGAGTTCTCCGC
CCTCCTGGCTCTTCTTGGAAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGCTAGAGCACGATAGAGGGAAACCCAACATTGGGAGTTAGAGTCTGCTCCCGCCCTTGCTG
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCC
TGCTCATCTCCAATAAAATAAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 64

MQGRVAGSCAPLGLLLVLHLPGLFARSIGVVEEKVSNFGTNLPQLGQPSSTGSPNSEHPQPAL
DPRSNDLARVPLKLSVPPSDGFPPAGGSVQWRWPPSWGLPAMDSWPPEDPWQMMAAAAEEDRLGEA
LPEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRRLPRSNLGGAGGKILSRP
PWSLIHRVLPDHPWGTILNPSVSWGGGGPGTGWGTRMPHPEGIWGINNQPPGTSWGNINRYPGGS
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPFVLRPPGSSWNIAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

FIGURE 65

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTC
TGGGCTGCCCCCTTGTCCTCCTTACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGA
CTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAA
TTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCACCCCTCCACCATGC
AAGATCTCAACACCATGTTGTCTGCAACACATGACAGCCATTGAAGCCTGTGTCTTCTTGGCCC
GGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAGCAGGCCCCCACCTC
CTGAGTGGCAATAAATAAAATTTCGGTATGCTG

FIGURE 66

MGSGLPVLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL
HHARSQHHVVCNT

Important features:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 37-41

N-myristoylation sites.

amino acids 15-21, 19-25, 60-66

10063712

FIGURE 67

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGC
CAGGTGCCCCGTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCC
TTCCTCGGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCG
CTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACAGACCACTTCTGC
AAATGAGAATAGCACTGTTTTCCTTCATCCACCAGCTCCAGCTCCGATGGCAACCTGCGTCCGG
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTCCTGGCTGTGGGGCTG
GCACTGTTGGTGGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCAGTAGCGA
GGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAAGGCT
GCCTGCCCATCTAGGTCCTCCTGCTGCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAA
GGCAGTGGCCTCTCTGGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAA
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGGCTATTCACCTTTATATATTTATATAAAATTAG
TAGTGAGATGTAAAAAAAAAAAAAAAAA

FIGURE 68

MANPGLGLLLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSSDGNLRPEAITAIIVFS
LLAALLLAVGLALLVRKLEKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 56-80

N-glycosylation site.

amino acids 36-40

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 86-90

Tyrosine kinase phosphorylation site.

amino acids 86-94

N-myristoylation sites.

amino acids 7-13, 26-32

FIGURE 69

GCCAGGAATACTAGAGAGGAACAATGGGGTTATTGAGAGGTTTGTTCCTCTTAGTTCTGTGCCTGCTGCACCAG
TCAAATACTTCCTTCATTAAGCTGAATAATAATGGCTTTGAAGATATTGTCATTGTTATAGATCCTAGTGTGCCAGAA
GATGAAAAAATAATTGAACAAATAGAGGATATGGTGACTACAGCTTCTACGTACCTGTTTGAAGCCACAGAAAAAGA
TTTTTTTTTCAAAATGTATCTATATTAATCCCTGAGAATTGGAAGGAAATCCCTCAGTACAAAAGGCCAAACATGAA
AACCATAACATGCTGATGTTATAGTTGCACCCCTACACTCCAGGTAGAGATGAACCATACACCAAGCAGTTCCACA
GAATGTGGAGAGAAAGGCGAATACATTCACTTCACCCTGACCTTCTACTTGGAAAAAACAATAATGAATATGGACCA
CCAGGCAAACTGTTTGTCCATGAGTGGGCTCACCTCCGGTGGGAGTGTGATGAGTACAATGAAGATCAGCCTTTC
TACCGTGCTAAGTCAAAAAAATCGAAGCAACAGGTGTTCCGCGAGGTATCTCTGGTAGAATAGAGTTTATAAGTGT
CAAGGAGGCAGCTGTCTTAGTAGAGCATGCAGAAATTGATTCTACAACAAACTGTATGGAAAAGATTGTCAATCTTT
CCTGATAAAGTACAACAGAAAAAGCATCCATAATGTTTATGCAAAGTATTGATTCTGTTGTTGAATTTTGAACGAA
AAAACCCATAATCAAGAAGCTCCAAGCCTACAAAACATAAAGTGAATTTTAGAAGTACATGGGAGGTGATTAGCAAT
TCTGAGGATTTTAAAAACACCATACCCATGGTGACACCACCTCCTCACCTGTCTCTCATGTCTGAAGATCAGTCAA
AGAATTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGTAAAGACCGCTAAATCGAATGAATCAAGCAGCA
AAACATTTCTGCTGCAGACTGTTGAAAATGGATCCTGGGTGGGATGGTTCACTTTGATAGTACTGCCACTATTGTA
AATAAGCTAATCAAATAAAAGCAGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATCCTCTGGGAGGA
ACTTCCATCTGCTCTGGAATTAATATGCAATTCAGGTGATTGGAGAGCTACATTCCTCAACTCGATGGATCCGAAAGTA
CTGCTGCTGACTGATGGGAGGATAACACTGCAAGTCTTGATTTGATGAAGTGAACAAAGTGGGGCATTGTTCAAT
TTTATTGCTTTGGGAAGAGCTGCTGATGAAGCAGTAATAGAGATGAGCAAGATAACAGGAGGAAGTCATTTTTATGTT
TCAGATGAAGCTCAGAACATGGCCTCATTGATGCTTTGGGGCTTTACATCAGGAAATACTGATCTCTCCAGAAAG
TCCCTTCAGCTCGAAAGTAAGGATTAACACTGAATAGTAATGCCTGGATGAACGACACTGTCAATTTGATAGTACA
GTGGGAAAGGACAGCTTCTTCTCATCACATGGAACAGTCTGCCTCCAGTATTTCTCTCTGGGATCCAGTGGAAACA
ATAATGGAAAATTTCAAGTGGATGCAACTTCCAAAATGGCCTATCTCAGTATTCAGGAACTGCAAAGGTGGGCACT
TGGGCATACATCTTCAAGCCAAAGCGAACCCAGAAACATTAATATTACAGTAACTTCTCGAGCAGCAAAATCTTCT
GTGCCTCCAATCAGCTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCGAGCCCAATGATGTTTACGCAGAA
ATTCTACAAGGATATGTACCTGTCTTGGAGCCAAATGTGACTGCTTTCAATTGAATCAGAAATGGACATACAGAAAT
TTGGAATTTTGGATAATGGTGACAGGCGCTGATCTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATAT
ACAGAAAATGGCAGATATAGCTTAAAGTTGCGGCTCATGGAGGAGCAAACTGCCAGGCTAAAATACGGCCTCCA
CTGAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGAAATTGAAGCAACCCGCCAAGACCTGAATTTGAT
GAGGATACTCAGACCACTTGGAGGATTTAGCCGAACAGCATCCGGAGGTGCATTTGTGGTATCACAAATCCCAAGC
CTTCCCTTGCTGACCAATCCCAAGTCAATCAGACCTTGATGCCACAGTTTATGAGGATAAGATTATTCTT
ACATGGACAGCACCAGGAGATAATTTGATGTTGAAAAGTTCACGTTATATCATAAGAAATAAGTGCAAGTATCTT
GATCTAAGAGACAGTTTGTGATGCTCTTCAAGTAAATACTACTGATCTGTACCAAGGAGGCCAACTCCAAGGAA
AGCTTTGCAATTAACAGAAAATATCTCAGAAGAAAATGCAACCCACATATTTATTGCCATTAAAGTATAGATAAA
AGCAATTTGACATCAAAGTATCCAACATTGCACAAGTAACTTTGTTTATCCCTCAAGCAAAATCCTGATGACATTGAT
CCTACACCTACTCCTACTCCTACTCCTACTCCTGATAAAAGTCATAATTCTGGAGTTAATATTTCTACGCTGGTATG
TCTGTGATTTGGTCTGTTGTAATTTGTTAACTTTATTTTAAGTACCACCATTTGAACCTTAACGAAGAAAAATCTTC
AAGTAGACCTAGAGAGAGTTTAAAAAACAACAAATGTAAGTAAAGGATATTCTGAATCTTAAATTCATCCCAT
GTGTGATCATAACTCATAAAAATAATTTTAAGATGTCGGAAGAGGATACTTTGATTAAATAAAACACTCATGGATA
TGTA AAAACTGTCAAGATTAATAATTAATAGTTTCATTTATTTGTTATTTTATTGTAAGAAATAGTGATGAACAAAG
ATCCCTTTTTCATACTGATACCTGGTGTATATTATTTGATGCAACAGTTTCTGAAATGATATTTCAAATTCATCAA
GAAATTAATAATCATCTATCTGAGTAGTCAAAATACAAGTAAAGGAGAGCAAAATAAACACATTTGGAAAAA
AA

FIGURE 70

MGLFRGFVFLVLVCLLHQSNSTFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTASTYLFE
ATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEY
IHFTPDLLLGGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRN
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFFPDQVTEKASIMFMQSIDSVVEFCNEKTHNQEAP
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRNLNR
MNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK
YAFQVIGELHSQLDGSEVLLLTGDGENTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG
SHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFL
ITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR
AANSSVPPITVNAKMNDVNSFSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA
GADSFKNMGVYSRYFTAYTENGRYSLKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPP
RPEIDEDTQTTLEDFSRTASGGAFFVVSQVPSLPLPDQYPPSQITDLATVHEDKIIILTWAPGDN
FDVGKVQRYIIRISASILDLRDSFDDALQVNTDLSPKANSKESFAFKPENISEENATHIFIAI
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVI
VNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 71

CTCCTTAGGTGGAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAGACCATACGTCCTCCCGGGCAGGGGTGA
CAACAGGTGTCATCTTTTGTATCTCGTGTGTGGCTGCCTTCTATTTCAAGGAAAGACGCCAAGGTAATTTT GACCCA
GAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCAAGTTATGCCAGGATTTACTAGAGAGTGTCA
ACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGGTTGGAGGAGAGAACCCTTGTGGGGCTGCGTTCTCTTAGCA
GTGCTCAGAAAGTGAATGCTGAGGGTGGACCAGAAGAAAGGAAAGGTCCTCTTGCTGTTGGCTGCACATCAGGAA
GGCTGTGATGGGAATGAAGGTGAAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAAA
AGTAGAGAAGTCTGCTGTGTGGTGGTAACTCCAAGAGGCAGAACTCGTCTAGAAGGAAATGGATGCAAGCAGCTC
CGGGGGCCCCAAACGCATGCTTCTGTGCTAGCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCTTTGAGGGATGCC
ACCGGTTCTGGACGCATGGCTGATTCCTGAATGATGATGGTTCGCGGGGGCTGCTTGCCTGGATTCCCGGGTGGTG
GTTTTGCTGGTGCCTCTGCTGTGCTATCTCTGCTGTACATGTTGGCTGCACCCCAAAGGTGACGAGGAGCAG
CTGGCACTGCCAGGGCCACAGCCCCACGGGGAAGGAGGGGTACCAGGCCGCTCTTCAGGAGTGGGAGGAGCAGCAC
CGCAACTACGTGAGCAGCCTGAAGCGGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGG
AATGGGCAGTACCAAGCCAGCATGCTGCTGGCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGCCGACCTC
CTGGCCTTCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGCAGTG
CCTTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCGAGGAGAAGCCTGTG
AGGAAGGACAAGCGGGATGAGTTGGTGAAGCCATTGAATCAGCCTTGGAGACCCTGAACAATCTGCAGAGAACAGC
CCCAATCACCGTCTTACACGGCTCTGATTTCTAGAAAGGGATCTACCGAACAGAAAGGGACAAGGGACATTGTAT
GAGCTCACCTTCAAAGGGGACCAAAACACGAATTCAAACGGCTCATCTTATTTGACACATTCAGCCCCATGAA
GTGAAAATGAAAAGCTCAACATGGCCAAACAGCCTTATCAATGTTATCGTGCTCTAGCAAAAAGGGTGGACAAGTTC
CGGCAGTTCATGCAGAAATTCAGGGAGATGTGCTTGGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGG
AAAGAACAAATAAATGAAGTCAAGGAATACTTGAAACACTTCAAAGCTGCCAATTCAGGAATTTACCTTCATC
CAGCTGAATGGAGAATTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAGGGGAAGCAACCTCCTC
TTTTTCTGTGATGTGGACATCTACTTCATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAG
GTATTTTATCCAGTTCTTTTCAGTCAGTACAATCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAA
CAGCAGCTGGTCATAAAGAAGGAACTGGATTTTGGAGAGACTTGGATTTGGGATGACGTGTGATTCGCTCAGAC
TTATCAATATAGGTGGTTTGTATCTGGACATCAAAGGCTGGGGCGGAGAGATGTGCACCTTTATCGCAAGTATCTC
CACAGCAACCTCATAGTGGTACGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAG
CTGACCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCACGGCCAGCTGGGCATGCTG
GTGTTCAAGCAGGATAGAGGCTCACCTTCGCAACAGAAACAGAACAGTAGCAAAAAACATGAACTCCAGAG
GAAGGATTTGGGGAGACACTTTTCTTCCCTTTTGCAATTACTGAAAGTGGCTGCAACAGAGAAAGACTTCCATAAA
GGACGACAAAAGATTTGACTGATGGGTGAGAGATGAGAAAGCCTCCGATTTCTCTGTTGGGCTTTTACAACAGA
AATCAAAATCTCCGCTTTCCTGCAAAAGTAACCCAGTTGACCCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTG
AGATTATAAGCCTAATGCTGTGGAGGTTTGTATGTTTACAATACACTGAGACCTGTGTTTTGTGCTCATTGA
AATATTCTATGATTTAAGAGCAGTTTGTAAAAAATTCATTAGCATGAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGCTCTAGTTTCTAGGAATGCTAAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTATATGATACT
AGTGAGTACATTAAGTAAAAATAAATGGACCAGAAAAAGAAACCATAAATATCGTGTATATTTTCCCCAAGAT
TAACCAAAAATAATCTGCTTATCTTTTGGTTGCTCTTTAACTGTCTCCGTTTTTTTCTTTTATTTAAAAATGCACT
TTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTACACTTTGCAAGCCTTACAAGAGAGCAAAAGTTGGCCTAC
ATTTTTATATTTTTTAAGAAGATACTTTGAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATGATGCCATAT
CCAAGGACATGCCAATGCTGATTCTGTCAGGCACTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTGTACT
AATACAGAGCTACAGATACTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATGAC
ACTTCTGCTTTACAGAAAAGGAACTCATTGAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACCATTTT
CTCCTCAGAAAGTAGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGTGTGAACCAACATCTCTTTTC
AAAACAGGGTGCTCCTCCTGGCTTCTGGCTCCATAAGAAGAAATGGAGAAAAATATATATATATATATATATATTGT
GAAAGATCAATCCATCTGCCAGAACTAGTGGGATGGAAGTTTTTGTACATGTTATCCACCCAGGCCAGGTGGAAG
TAACTGAATTTTAAAAATAAATACAGTTAAATAGAGTGGTTTCTTCAATCATGTGAAAATATTAGCCAGCCAG
ATGCATGAGCTAATATCTCTTTGAGTCTGCTTCTGTTGCTCACAGTAAACTCATTGTTTAAAGCTTCAAGAAC
ATTCAAGCTGTGGTGTGTTAAAAAATGCATGTATGATTGTACTGGTAGTTATGAAATTTAATTAACACAGG
CCATGAATGGAAGTGGTATTGCACAGCTAATAAATATGATTGTGGATATGAA

FIGURE 72

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSPGKEGYQAVLQWE
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFLHSQVDK
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIESALETNNPA
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAN
TLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNTQPGKKVFYFVLFVSQY
NPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYR
KYLHSLIVVRTPVRLFHLWHEKRCMDLTPQYKCMQSKAMNEASHGQLGMLVFRHEIEAHL
RKQKQKTSSKKT

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 315-319, 324-328

N-myristoylation sites.

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

Amidation site.

amino acids 377-381

FIGURE 74

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPLPALQ
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQINSEAT
FAELHIVHYDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP
FNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGITLFSTEEEPSKLLV
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS
VVFTSAQATTEA

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 75

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGTGTC
TCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGTCCTACA
ATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTTCATCACAA
ATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCTGTTTCCATGCAACAAATATACTCCAATCTGA
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAACCAC
ACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTCGTCCC
AGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGATCAATCAT
CAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGTGTTCCTTTTT
TCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACACCCAGCAAATTT
GATTTTGATTTATGGAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGAAAAATCGTGATTA
ACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGATATGAGTTTACTGGGA
AAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACTGAGGCCCCCTCAGGA
GGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGAATTTTTTGTGACTCTGAAG
AAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCGGATAAA
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTTGTGCGGGCCCTGAAGAGCAGGA
GCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAG
TCTTGGGCCCCGAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCG
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCTGGTCGACTGGGA
TCCCCAAACTGGCAGGCTGTGTATTCCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCG
AGCCTTCTGAGGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGCT
CCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGTTATA
TGTGCAGATGGAACTGATGCCAACTTCCTTTTGCCTTTTGTTTCTGTGCAACAAGTGAG
TCACCCCTTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGTTTGTCACTGT
CTGTGAGAATTACTTATTTCTTTCTATTCTCATAGCACGTGTGTGATTGGTTCATGCATGTA
GGTCTCTTAACAATGATGGTGGGCCCTCTGGAGTCCAGGGCTGGCCGGTTGTTCTATGCAGAGAA
AGCAGTCAATAAATGTTTGCAGACTGGGTGCAGAATTTATTAGGTGGGTGT

FIGURE 76

MSYNGLHQRVFKELKLLTLCSSISQIGPPEVALTTDEKSSISVVLTAPEKWKRNPEDLPVSMQQIY
SNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLK
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFEDKRFFVPAEK
IVINFITLNISSDKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFC
DSEENTEGTSLTQQESLSRTIPDPKTVIEYEYDVRTTDCAGPEEQELSLQEEVSTQGTLLSQA
ALAVLGPQTLQYSYTPQLQDLDPQAQHTDSEEGPEEEPSTTLVDWDPTGRLCIPSLSSFDQDS
EGCEPSEGDLGEGELLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 77

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACAC
CTGGGAAGATGCGCGCCCGTGGACCTTCACCCCTCTCTGTGGTTTGCTGGCAGCCACCTTGATC
CAAGCCACCTCAGTCCCAGTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGC
GGGAAAAGCCAGCCGAGGCATCCCTGTGTGGGCAGCCTGGTGAACACCGTCTGAAGCACATC
ATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCCCTCGGCCAATGACCA
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAAGACCA
TCGTGGAGTTCCACATGACGACTGAGGCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGC
CCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTCTGTGA
TAAGTCTCCTTCTGTGGTGAAGCCTTAGCTAAGCAGGTATGAACCTCCTAGTGCCATCCCTGC
CCAATCTAGTGA AAAACCAGCTGTGTCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGAC
CTCCTGCAGCTGGTGAAGGTGCCATTTCCCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTGA
TCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAAGTTGTTGGACTCACAGGGAA
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCG
TTCAGCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTGATGGTCTGTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGC
TGATCAATGAAAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGAC
ACTCCCGAGTTTTTTATAGACCAAGGCCATGCCAAGGTGGGCCAACTGATCGTGTGGAAGTGTT
TCCCTCCAGTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGT
TTTACACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTG
ATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA
CTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTGAAGG
CCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCTCC
TTGTGGA AACCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGG
GTCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTG
CCTGTGAAAAA

FIGURE 78

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAMREK
PAGGIPVLGSLVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLLDSQGKVT
KWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPEEFMVLLDSVLPESAHLKSSIGLIN
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPLFTLGIEASSEAQFYT
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSVLKALG
FEAAESSLTKDALVLTASLWKPPSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 79

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC
TTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCT
CTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTGGGCACACTGGTTGCCAT
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTCGGTGCCAGCATTGTGACAGCAGTTGGCTTCT
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAGTGTGACATCTATAGC
ACCCCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT
CTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCCAGGAATCCC
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCT
ATTCTGTGCTGGAATCTTCATGGGATCCTACGGGACTTCTACTCACCACCTGGTGCCTGACAG
CATGAAATTTGAGATTGGAGAGGCTCTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAG
CTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGAGAAATCGCTCCAACCTACTACGATGCCTAC
CAAGCCCAACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGA
GTTCAATTCCCTACAGCCTGACAGGGTATGTGTGAAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTG
GGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGG
GCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCC
TCACCTTGCTGCTCCCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTTAAGCCA
GGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACA
TCCCCTGACTGACCCTCTGTGATCAAAGACCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATT
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTC
CCTCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCCTCTTGTATGACTCCACAGTGTCCA
GACTAATTTGTGCATGAACTGAAATAAAACCATCTACGGTATCCAGGGAACAGAAAGCAGGATG
CAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

FIGURE 8o

MASLGLQLVGYYLGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGITQCD
IYSTLLGLLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL
LGFIPVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSSQRNRSNYY
DAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 81

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTC
CCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCCCT
GCCACCGCTGCTTCTTGCCCTTCTCCGACCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGG
GTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGG
ACCAGCGGCTGACCTGGGGAAAGGATGGTTCCCGAGGTGAGGGTCTCTCCTCCTTGTCTGGGA
CTCGCGCTGCTTGGTTCCTTGGACTCCACGCTCGAGCCGCCCAGACATGTTCTGCCTTTT
CCATGGGAAGAGATACCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT
ACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCT
GTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACAC
TCCCTCTGGACTCCGGGCCCCACCAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAG
AGATCTTCAGTGCCCATGAGCTGTTCCCTCCCGCCTGCCCAACCAAGTGTGTCTCTGCAGCTGC
ACAGAGGGCCAGATCTACTGCGGCCTCACAACCTGCCCCGAACCAAGGCTGCCAGCACCCCTCCC
ACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGTGCAATCGGATGAAGAGGACA
GTGTGCAGTTCGTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGTGCTGGGAGAAAG
AGAGGCCCGGGCACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCCTGAAGGAGAAACATAAGAAAGCCT
GTGTGCATGGCGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGC
CCCTTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC
CACCGAGTACCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGG
ACAAAGCAGACCCTGGCCACAGTGTGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTC
CTCGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTTCGCTTTGCCCTGGAACACGAGGC
CTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAGAGAG
GTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAG
GAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCCT
GGAACGTCTTCCCTAGCCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAG
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTTATTATATATTAATAAA
TAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 82

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCPEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHEL
PSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR
HPQDPCSSDAGRKRGPPTAPGTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTY
HGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKVAGKCKICPEDKADPGHSE
ISSTRCPKAPGRVLVHTSVSPDNLRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH
SQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEGHGQSRQSDQDITKT

Signal peptide:

amino acids 1-25

FIGURE 83

GACAGCTGTGCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAGAGCCTCTCC
GTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCATCCGTCACCTCTCCTGTCA
TCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTTGGTTCTGAGTC
TCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCCTGGTGGGGGAG
GACGCAGCATTCTCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGG
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATC
AAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTACT
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCATCTGGGAGCT
ACAGGTGTGAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTTGATAGAGACATCCAGCTAC
TCTGTGCTCCTCGGGCTGGTTCCCCCGCCCCACAGCGAAGTGGAAGGTCCACAAGGACAGGATTTGTCC
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTGATGTGGAGATCTCTGTGACCGTCCAAGAGAA
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAG
GAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTA
TTTTTTGGCATTGTTGGACTGAAGATTTCTTCTCCAAATTCAGTGGAAAATCCAGGCGGAATGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCTGGATCCAG
AGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACCTAACCCTATAGAAAAGCTCCCCAGGAGGTG
CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCAGGGAACATTA
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGA
AGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTT
ACATTAATCCCCGTTTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTA
TGAGTGTGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGTTTG
AAGGCTTATTGAGGCCCTACATTGAGATATCCGTCCTATAATGAGCAAAATGGAACCTCCCATAGTCATCTGC
CCAGTCAACCAGGAATCAGAGAAAGAGGCCTCTTGGCAAAGGGCTCTGCAATCCAGAGACAAGCAACAG
TGAGTCTCTCTCACAGGCAACCACGCCCTTCTCTCCAGGGGTGAAATGTAGGATGAATCACATCCCACAT
TCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA
GATGAAGGGGACTGGCCTGTCCACATGGGAGTCAGGTGTCTGCGTGCCTGAGCTGGGAGGGAAGAAGG
CTGACATTACATTTAGTTTGTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAG
AACCGTCAGGAATCCCCTCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG
ATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACATTTTCAAGTAAAAAA

FIGURE 84

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFSCLSPKTNAEAMEVRFFRGQFSSVH
LYRDGKDQPFMQMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISQSYQKAIWELQ
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRTAKWKGPGQDLSTDSRTNRDMHGLFDVEISL
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK
FQWKIQAELDWRRKHGQAEIRDARKHAVEVTLDPEAHPKLCVSDLKTVTHRKAPQEVPHSEKRF
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRKEYVTLSPDHGYWVLRNLNGEHLFT
LNPRFISVFPRTPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLRPYIEYPSYNEQNGT
PIVICPVTQESEKEASWQRASAIPESTNSSESSQATTPFLPRGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 85

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCT
GCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCCGTGA
CGGTGCAGGAAGGCCTGTGTGTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATT
TACCCTGGCCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGGCCAATACAGACCAGGATGCTCC
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACCGATTCCACCTCCTTG
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGATGCGGGGAGA
TACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCTGTGAA
TGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCCCTGGAGTCGGCTGCCCCC
AGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATA
GGGACCTCCGTGTCCCCCTGGACCCCTCCACCACCGCTCCTCGGTGCTCACCCCTCATCCCACA
GCCCCAGGACCATGGCACCAGCCTCACCTGTGAGTGACCTTCCCTGGGGCCAGCGTGACCACGA
ACAAGACCGTCCATCTCAACGTGTCCTACCCGCTCAGAACTTGACCATGACTGTCTTCCAAGGA
GACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCACTCCAGAGGGCCAGTCTCT
GCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCTGCCAGGCTGAGCCTGAGCTGGA
GAGGCCTGACCTGTGCCCTCACAGCCCTCAAACCCGGGGTGCTGGAGCTGCCCTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCT
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGAAGTCAAGGGGTGGTTCGGGGAGCTGGAG
CCACAGCCCTGGTCTTCCTGTCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAA
TCGCAAGGCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTTC
AGCCTCTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAG
CTTCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGTG
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG
ATGAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCA
GAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG
TGCAGAGTGAAAAGCACACAGGCTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCC
TCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

FIGURE 86

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIIYPGPVVHGYWFREG
ANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNY
KHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVSPDPSTTRS
SVLTLPQPQDHGTS LTCQVTFPGASVTTNKTVHLNVSYPPQNLMTVFQGDGTVSTVLGNGSSL
SLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNP
LGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRKKSARPAAGVGDGIE
DANAVRGSSASQGPLEPWAEDSPPDQPPPASARSSVGEGELQYASLSFQMVKPWDSRGQEATDTE
YSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 87

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTAC
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGT
TCTTCGTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTTGA
TGGCCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCTGTGACATGACCTCTG
GGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG
GGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAACTGGGC
CAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCTGGCTACT
ACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG
AGAAACAGCTCCCTGCTGAGGTACCGCACGGCACTGGCTTCCTCCAGACACTGGGACATAATCT
GTTTGGCATCTACCAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCC
CGGTGATCCCTGTGGTCTATGATTTTGGCGACGCCAGAAAACAGCATCTTATTACTCACCCAT
GGCCAGCGGGAATTCAC TGCGGGATTTGTTTCAGTTCAGGGTATTTAATAACGAGAGAGCAGCCAA
CGCCTTGTTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG
GATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACCTCATGTTGGTTACAGCAGCAGCCGTGAGATAAAGTGGAGCTGTGCTTCTATTCTATCG
TTGAGAGTTTTGTGGGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAA
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGA
AAAAA

FIGURE 88

MNQLSFLFLIATTRGWSSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI
YQTFCDMTSGGGGWTTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAAT
SDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYG
EGKCWTDNGPVIPVVYDFGDAQKTASYSPYGQREFTAGFVQFRVFNNERAANALCAGMRVTGCN
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSSREITEAAVLLFYR

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation site.

amino acids 163-167

Glycosaminoglycan attachment sites.

amino acids 74-78, 289-293

N-myristoylation sites.

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

FIGURE 89

CTAGATTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGAC
CGCCGCCCTTGTCCTCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACG
CTCCTGGCGCATCTGGTGGTCGTACACCTTATTCTGGTCCCGGACAGCAACATACAGGCCTG
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGGTGGCCGCGCTCT
CTGTACCCCTGGGCCCTCTTTGCAGTGGAGCTGGCCGGTTTCTCTCAGGAGTCTCCATGTTCAAC
AGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTTCAT
ATTGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCCTCCAGCTG
TCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAAGAAACCCCTTCTGATTACCTTCA
TGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCTGGAAGAAGGAAG
GCATAGGCTTCGGTTTTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACG
TCTTGAGTCTGGGATTATCCGCATTGTATTAGTGCTTTGTAATAAAATATGTTTGTAGTAACA
TTAAGACTTATATACAGTTTtaggggacaattaaaaaaaaaaaa

FIGURE 90

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFV
TVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 91

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC
TCGCTGCTGCTTCGTGTTCTTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATG
GTCCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCT
CGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATCCAATCTCCTAGGGCTGCT
GGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCCCGAACCACAGCCCCC
CACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCCAACATCAAGACGGTG
GCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTCCACTT
CCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAG
AGTTCACACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATG
GAGTGGGAGAAGGTAGAACGGGGCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTG
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTG
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACTAC
CATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGCCAGGGC
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGGGTGGGCCCTC
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGA TAGATCACAGGAGCACTGG
AGGAGGAGTGGGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGG
TCCCCGAGGCCTGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGC
CCTTGGTTCTTGCCATCTTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACA
GCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGGG
GCCAGAGGAGCTCTCCAGCCCTGCCCTAGTGGGCGCCCTGAGCCCCCTGTCTGTGTCTGAGCATGG
CATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTCCAGC
CAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG
GCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCCACAGCCCATC
CGCGTGCTGTGTCTCCCTCTTCCACCCCAACCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCG
GAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACGGGGTTCTCCGGATCTGGATGGCGC
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGCCGGGCCGAGAGCATGTGCTGGATCTGTTT
TGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGAAACCGCTGATTGCTGACTTT
TGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 92

MLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTF
SVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDP
AKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 93

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCC
CTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTT
CTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTGGTTCATGGCAAGAGTCATTATTGACAACA
AAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTGTCTATATCCAAGAA
ATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTTGAAGAGTATAAACCC
AGGTGAGACAGCACCTCTATGCGACTGCTGGCCTATGTTTCTGGCTGGGCTTTGGAATCATGA
GTGGAGTATTTTCTTTTGAATACCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCATTTCAT
GGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGT
ATTCTGGGGCATGTATTTTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTT
TCCTGACCCACCTGCTGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCG
TCAGCATTTATAATCCTGGTGCTCATGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCG
AAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGAACTTCTTCTTTACAACCAGCGCTCCAGAT
AACTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCT
TTTTCTGAAATCCCTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 94

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV
FSFVNTLSDSLPGTVGIHGDSPOFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLT
HLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSLKCLLCQDKNFLLYNQSR

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 95

AATTTTTCACCAGAGTAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTTGCCTCGTG
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTCTAGGATCAAC
TCGGTCATTACCACAGCTCAAACCTGCTTTGGGACTCCCTCCCACAAAACCTGGCTCCGGATCAGG
GAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTTCCTTCTTTAAGTCTGATACCATTAAAC
CAGATGCTCACACTGGGGCCAGATCTGCATCTGTAAATCCTGCTGCAGGAATGACACCTGGTAC
CCAGACCCACCCATTGACCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC
CAATTTTGTGCACACAACCTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATTGCCACAAATC
TTCACGAGCCTCATCATCCATTCTTGTTCCTGGGAGGCATCCTGCCACCAGTCAGGCAGGGGC
TAATCCAGATGTCCAGGATGGAAGCCTTCCAGCAGGAGGAGCAGGTGTAAATCCTGCCACCCAGG
GAACCCAGCAGGCCGCCCTCCCAACTCCCAGTGGCACAGATGACGACTTTGCAGTGACCAACCCCT
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA
GTAAGCTGTTCAAATTTTTTCAACTAAGCTGCCTCGAATTGGTGATACATGTGAATCTTTATC
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTTAGAAGAAATTAATCTTAATT
TACCTGAAAATATTCTTGAAATTTAGAAAATATGTTCTATGTAGAGAATCCCAACTTTTAAAAA
CAATAATTCAATGGATAAATCTGTCTTTGAAATATAACATTATGCTGCCTGGATGATATGCATAT
TAAACATATTTGGAACCTGCAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 96

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGFDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLSIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 97

GCTCAAGTGCCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT
 CTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGGCGCTGGAGGGCCCTGTCTTGACCATG
 GTCCCTGCCCTGGCTGTGGCTGCTTTGTGTCTCCGTCCCCAGGCTCTCCCCAAGGCCAGCCTGC
 AGAGCTGTCTGTGGAAGTTCAGAAAACTATGGTGGAAATTTCCCTTTATACCTGACCAAGTTGC
 CGCTGCCCCGTGAGGGGGCTGAAGGCCAGATCGTGTCTGTCAGGGGACTCAGGCAAGGCAACTGAG
 GGCCCATTTGTATGGATCCAGATTCTGGCTTCTGTCTGGTGACCAAGGGCCCTGGACCGAGAGGA
 GCAGGCAGAGTACCAGCTACAGGTACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGGTCCAC
 AGCCTGTGCTTGTGCACGTGAAGGATGAGAAAGACCAAGGTGCCCCATTTCTCTCAAGCCATCTAC
 AGAGCTCGGCTGAGCCGGGGTACCAGGCTGGCATCCCCCTTCTCTTCTTGGGCTTCAGACCG
 GGATGAGCCAGGCACAGCCAACCTCGGATCTTCGATTCCACATCCTGAGCCAGGCTCCAGCCCCAGC
 CTTCCCCAGACATGTTCCAGCTGGAGCCTCGGCTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGC
 ACCAGCCTTGACCACGCCCTGGAGAGGACCTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGA
 CCAGGCCTCAGGCCACCAAGGCCACTGCCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGT
 CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGCACCACATGGCCCAAGGTA
 CACTGGAGTGGGGTGTATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCTTTGAAGTGAA
 TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGGCCAGGCTGAGTACCTGCTCC
 AGGTGCGGGCTCAGAATTTCCATGGCGAGGACTATGCGGGCCCTCTGGAGCTGCACGTGCTGGTG
 ATGGATGAGAATGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT
 CAGTCCACCAGGTACTGAAGTGACTAGACTGTGAGCAGAGGATGCAGATGCCCCCGGCTCCCCCA
 ATTTCCACGTTGTGTATCAGCTCCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTC
 CAGGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGGTGCTCCCACTCCGAGCAGGCCAGAACAT
 CCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCACGTGTGAAG
 TCGAAGTCGAGTCACAGATATCAATGATCACGCCCCGTGAGTTCATCACTTCCAGATTGGGCCT
 ATAAGCCTCCCTGAGGATGTGGAGCCCGGGACTCTGGTGCCATGCTAAACAGCCATTGATGCTGA
 CCTCGAGCCCGCCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACAGAAGGGACTTTTG
 GCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG
 GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGAAGCTGGTGGGGCCAGGCC
 AGGCCCTGGAGCCACCGCCACGGTGAAGTGTGCTAGTGGAGAGAGTGTGACACCCCCCAAGTTGG
 ACCAGGAGAGCTACGAGGCCAGTGTCCCATCAGTGCCCGAGCCGGCTCTTCTGCTGACCATC
 CAGCCCTCCGACCCCATCAGCCGAACCTCAGGTTCTCCCTAGTCAATGACTCAGAGGGCTGGCT
 CTGCATTGAGAAATTTCTCCGGGAGGTGCACACCGCCAGTCCCTGCAGGGCGCCAGCCTGGGG
 ACACCTACACGGTGCTTGTGGAGGGCCAGGATACAGCCCTGACTCTTGCCCCGTGCCCCCCCAA
 TACCTCTGCACACCCCGCCAAGACCATGGCTTGATCTGTGAGTGGACCCAGCAAGGACCCGATCT
 GGCCAGTGGGCACGGTCCCTACAGCTTACCCCTTGGTCCCAACCCACGGTGCACCGGATTGGC
 GCCTCCAGACTCTCAATGGTTCCCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGT
 GAACACATAATCCCGTGGTGGTGCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGAT
 CGTGTGTCGCTGCAACGTGGAGGGGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCCA
 CGAAGCTGTGCGCAGTGGGCATCCTTGTAGGCACCTGGTAGCAATAGGAATCTTCCTCATCCTC
 ATTTTCACCCACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGGCCCT
 GAAGGCGACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCTCTGGCTCCATCTGAG
 TCCCCTGGGAGAGAGCCAGCACCCAAGATCCAGCAGGGGACAGGACAGAGTAGAAGCCCCCTCCA
 TCTGCCCTGGGGTGGAGGCACCATCACCATCACCAGGCATGTCTGCAGAGCCTGGACACCAACTT
 TATGGACTGCCCCATGGGAGTGCTCCAAATGTGAGGGTGTTTGCCCAATAATAAGCCCCAGAGAA
 CTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 98

MVPAWLWLLCVSVPQALPKAQAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT
EGPFAMDPDPSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVPHFSQAI
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQSPDMFQLEPRLGALALSPKG
STSLDHALERTYQLLVQVKMDGDQASGHQATATVEVSI IESTWVSLEPIHLAENLKVLYPHHMAQ
VHWSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDIAAPLELHVL
VMDENDNVPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPEPEDGVEGRA
FQVDPTSGSVTLGVPLPRAGQNILLVLAMDLAGAEGGFSSTCEVEVAVTDINDHAPEFITSQIG
PISLPEDVEPGTLVAMLTADADLEPAFRIMDFAIERGDTGTFGLDWEPPDSGHVRLRLCKNLSY
EAAPSHEVVVVQSVAKLVGPGPGGATATVTVLVERVMPPPKLDQESYEASVPISAPAGSFLLT
IQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALT LAPVPS
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRLQTLNGSHAYLTALHWVEP
REHIIPVVVSHNAQMWQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTTLVAIGIFLI
LIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 99

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTG
AGTCCAAGATTCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTA
TCTCTTCACCTTCAAGTCCCCCTTTCTCAAGAACTCCTCTGTCTTTGGCCCTCTAAAGTCTTGGTAC
ATCTAGGACCCAGGCATCTTGCTTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG
TTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGCAACAAATCCAATGAGACTAGCACC
TCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCACCAACTCTGGGTCCAG
TGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGGGGTCA
GCATAGTCACCAACTCTGAGTTCCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAG
TTCAGCACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCACT
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCC
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACT
GCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCA
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAG
TCCAGCACGACCTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGTAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCGGCACAGCCACCAACT
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCTCC
AGTGGGGCCACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGGCCACACAGCCAC
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA
CCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACA
GCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAG
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCA
ACACAGCCACCAACTCTGGGTCCAGTGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGA
ATGCACACAACTTCCCATAGTGATCTACTGCAGTGAAGGCAAGCCTGGTGGGTCCCTGGT
GCCGTGGGAAATCTTCTCATACCCCTGGTCTCGGTTGTGGCGGCCGTGGGGCTCTTTGCTGGGC
TCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGTCTACCACCT
CATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCACAGGCCAG
GTGGAGTCCCTAACTGGTTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGA
ACAGCGGGCCCTGAGCAGCCCCGGAAGCAAGTGCCGCTTCTTCAGGAAGGAAGAGACCTGGGCA
CCCAAGACCTGGTTTCCCTTTCATTTCATCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAA
AATCTTGAAGAAGGTATTCCTCACCTTTCTTGCTTTACCAGACACTGGAAAGAGAATACTATAT
TGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTTG
CCCCGGGGTGGGTATCTAGCTCTGAGATGAATCAGTTATAGGAGAAAACCTCCATGCTGGACTC
CATCTGGCATTCAAAATCTCCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 100

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNESSTTSSGASTATNESSTPSS
GASTVTNSGSSVTSSGASTATNESSTVSSRASTATNESSTLSSGASTATNSDSSTTSSGASTA
TNSESSTTSSGASTATNESSTVSSRASTATNESSTTSSGASTATNESRTTNGAGTATNES
STTSSGASTATNSDSSTVSSGASTATNESSTTSSGASTATNESSTTSSGASTATNSDSSTTSS
GAGTATNESSTVSSGISTVTNESSTPSSGANTATNESSTTSSGANTATNESSTVSSGASTA
TNSESSTTSSGVSTATNESSTTSSGASTATNSDSSTTSSEASTATNESSTVSSGISTVTNES
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA
AVGLEAGLFFCVRNLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFRRPVSSI
AMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 101

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCGCGACGGAGGTTGTGACCCCTA
CGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGGCGTGCCCTGCTGTGCACAGGTG
GGAGGCTGGAATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCAACAAAT
GGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCATGGTCAATT
AACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCTTTGGAATCAT
GGTGTGATGGAAAGGGATTACTTTTATACTGACTCTGTTTTGGGGAAGCTTTTTTGGGAAGCATTT
TCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAACCCATCTTGGTATCGCTGGATCAACAAC
CGCCTTGTGGCAACATGGCTCACCCTACCTGTGGCATTATTGGAGACCATGTTTGGTGTAAAGT
GATTATAACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTCATTATCATGAACCATCGGACAA
GAATGGACTGGATGTTCCGTGGAATTGCCTGATGCGATATAGCTACCTCAGATTGGAGAAAATT
TGCCCTCAAAGCGAGTCTCAAAGGTGTCTGGATTGGTTGGGCCATGCAGGCTGCTGCCATATAT
CTTCATTATAGGAAATGGAAGGATGACAAGAGCCATTTCGAAGACATGATTGATTACTTTTGTG
ATATTCACGAACCACTTCAACTCCTCATATTCAGAGAGGACTGATCTCACAGAAAACAGCAAG
TCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTCAGAAATATGAATATGTTTTACATCCAAG
AACTACAGGCTTTACTTTTGTGGTAGACCGTCTAAGAGAAGGTAAGAACCTTGATGCTGTCCATG
ATATCACTGTGGCGTATCCTCACAACATTCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTTT
CCCAGGGAAATCCACTTTTACGTCACCGGTATCCAATAGACACCTCCCCACATCCAAGGAGGA
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAG
GGGAGAAGAATTTTTATTTTACCGGACAGAGTGCATTCCACCTTGCAAGTCTGAAGTCTGAGGCTC
CTTGTGGTCAAATTGCTCTCTATACTGTATTGGACCCTGTTTCAAGCCCTGCAATGTGCCTACTCAT
ATATTTGTACAGTCTTGTAAAGTGGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGA
GAATATTTGGTGGACTGGAGATCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACAT
TTAAATTCAAAGAAAAATGAGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTG
GAAATGTTCTAAACCTTTCTAAGCTCAGATGCATTTTGCATGACTATGTCGAATATTTCTTACT
GCCATCATTATTTGTAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTT
TTTAATCTCTGAATGTAATTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTT
GGGCCAGAATATTATTAAACAATCATCAGGCTTTTAA

FIGURE 102

MHSRGREIVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSI FMLS P
FLPLMEFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM
FLWNCIMRYSYLRLKICLKASLKGVPFGFWAMQAAAYIFIHRKWDDKSHFEDMIDYFCDIHEP
LQLLIFPEGTDLTENSKSRSNFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA
YPHNIPQSEKHLQGDFFPREIHVFHVRYPIDTLPTSKEDQLWCHKRWEEKEERLRSFYQGEKNF
YFTGQSVIPCKSELRLVLVVKLLSILYWTLFSPAMCLLIYLSLVKWFIIITIVIFVLQERIFGG
LEIIEIACRYRLHKKPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 103

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGACC
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCCACAGGAATA
TCCATGGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTGGCAAGT
CACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCTGCTCCCTCT
TTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTCTTTCAGGAATCAGTTCCATGCTGTGGTC
CACCTCTACAGAGATGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCGAGGGAGAAGTGA
GTTTGTGAAGGACTCCATTGTCAGGGGGCGTGTCTCTAAGGCTAAAAACATCACTCCCTCGG
ACATCGGCCTGTATGGGTGCTGGTTCACTTCCAGATTTACGATGAGGAGGCCACCTGGGAGCTG
CGGGTGGCAGCACTGGGCTCACTTCCCTCTCATTTCATCGTGGGATATGTTGACGGAGGTATCCA
GTTACTCTGCCCTGCTCTCAGGCTGGTTCCCCCAGCCACAGCCAAGTGGAAAGGTCCACAAGGAC
AGGATTTGTCTTCAGACTCCAGAGCAATGCAGATGGGTACAGCCTGTATGATGTGGAGATCTCC
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGA
GGTGGATCCAAGGTATTGATAGGAGAGACGTTTTCAGCCCTCACCTTGGCGCTGGCTTCTA
TTTTACTCGGGTACTCTGTGGTGCCCTGTGTGGTGTGTCATGGGGATGATAATTGTTTTCTTC
AAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAG
AGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCG
TTTCTGATCTGAAAACGTAAACCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGA
TTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGA
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGACA
ATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTT
ACATTCAATCCCATTTTATCAGCCTCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCT
GGACTATGAGGGTGGGACCATCTCCTTCTCAATACAAATGACCAGTCCCTTATTTATACCTGTC
TGACATGTGAGTTGAAGGCTTGTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAG
GGGACTCCCATATTATATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGC
CCACACCCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCGACAGGTGGCCCCAGCTTCTCT
CCGGAGCCTGCGCACAGAGAGTCACGCCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCC
TGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGATTGGCCTGACCCTGTGGGAG
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAA
CTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGG
ACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGACAGGT
TGAGGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCACCATAAACTCTGTT
TGCTTATCCCATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACACC
TGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT
TACCTGATACCAAACAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCATATCC
CTCATTAACACAGACACAAAATTCTAAATAAAATTTAACAAATTAACTAAACAATATATTTA
AAGATGATATATACTACTCAGTGTGGTTGTCCACAAATGCAGAGTTGGTTTAAATATTTAAAT
ATCAACCAGTGTAAATCAGCACATTAATAAAGTAAAAAGAAAACCATAAAAA

FIGURE 104

MAFVLILVLSFYELVSGQWQVTGPGKEVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH
LYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR
VAALGSLPLISIVGYVDGGIQLLCLSSGWFPPQPTAKWKGPQGDLSSDSRANADGYSLYDVEISI
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALCGVVMGMIIVFFK
SKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSFNNGYWVLRLLTTEHLYFT
FNPHFISLPPSTPPTRVGVELDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG
TPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 105

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAGGAAAAGAG
 TTTGTTGGGAACCTTGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGCTCTGGCAGTGTGCATTGGA
 CTCAGTGTTCATTATGTGAGATATAATCAAAGAAGACCTACAATTACTATAGCACATTGTCATTTACAAC
 TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAACAATTTTACAGAAATGAGCCAGAGACTTGAAT
 CAATGGTGAAAAATGCATTTTATAAATCTCCATTAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTC
 AGTCAACAGAAGCATGGAGTGTGGCTCATATGCTGTTGATTGTAGATTTCACTCTACTGAGGATCCTGA
 AACTGTAGATAAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG
 ATCCTCACTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGGA
 ACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAAGTAGAAGAGGGTGAATG
 GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTAATGCCACATGGC
 TTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAGATGGACTGCTTCCTTTGGAGTAACA
 ATAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAATAATTGTCCATGAAAATACAAACACCCATCACA
 TGACTATGATATTTCTCTTGAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCT
 TCCCTGATGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAAT
 GATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACTTGAATGAACC
 TCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAACAGATGCAT
 GCCAGGGTGACTCTGGAGGACCCTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGCTGGAATAGTG
 AGCTGGGGAGATGAATGTGCGAAACCCCAACAGCCTGGTGTTTATACTAGAGTTACGGCCTTGCGGGACTG
 GATTACTTCAAAAATGGTATCTAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTTG
 GGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCA
 ATAAACTGTTTGCTTGATGCATGTATTTCTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA
 GATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAATACAATATTAC
 ATTACAGCCTGTATTCATTTGTCTCTAGAAGTTTGTGTCAGAAATTTGACTTGTGACATAAATTTGTAAT
 GCATATATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTCAGCAAAATATCCATTT
 TCAAGGTGCAGACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCCTACATTTTATTGGCACAGAA
 AAGTATTAGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTATTATGAAAGGTCAAGCAAAGACA
 GCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAAGTAAGTTAAGGAAGTCCAGAAAGAAGCCAAG
 ATATATCCTTATTTTCATTTCCAAACAACCTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCT
 ATAATAATTATACAACTTCATGCAATGTACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTG
 TTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

FIGURE 106

MMYRPDVVRARKRVCWEPWVIGLVI F ISLIVLAVCIGLTVHYVRYNQKKTNYNSTLSFTTDKLY
AEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFHSTED
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL
RRIIVHEKYKHPSHDYDISLAELSSVPYPTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS
QNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLVSSDARDIWYLAG
IVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 107

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCCTG
CCCCGATGAGCCCCCGCGTCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCCCAGC
GCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTCTCCCTT
ACGGGGCTCACAATGCCAGAGAAGATCCGTGAAGTGTCTGCGCTGCCCTGCTCTACGCCCTCAA
TCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGGGACTACCTAA
ATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTGACTTACTTTCTT
GTGGTTCATCCGGTCATGATTGCTGTTTCTGTTTCTTATCATTGTGGGGATGTTAGGATATTG
TGAACGGTGAAAGAAATCTGTGCTTCTGCATGGTACTTTGGAAGTTGCTTGTCAATTTCT
GTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATGGTTCCAGTACAATGGTCA
GATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCA
TGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTAGTATATTTCACTGACTGGTTGG
AAATGACAGAGATGGACTGGCCCCCAGATTCTGTGCTGTGTAGAGAATTCAGGATGTTCCAAA
CAGGCCCCACAGGAAGATCTCAGTGACCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCCTT
TTTGAGAGGAACCAACAACATGCAGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAA
TCCTGGCCATGATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGG
ACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCTGTCCCTCAGTAGAAT
GTTGAAACCAAGCCTGTCAAGAACTTTTGAACACACATCCATGGCAAACAGCTTTAATACACACT
TTGAGATGGAGGAGTTATAAAAGAAATGTCACAGAAGAAAACACAAACTTGTATTATTGGACT
TGTGAATTTTTGAGTACATATCTATGTGTTTCAGAAATATGTAGAAAATAAAATGTTGCCATAAAA
TAACACCTAAGCATATACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTTCATGTCATAAGTC
ACCACCTGGACAATAATTGATGCCCTTAAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCC
TGTGTATGACTTTTACTGAACACAGTTATGTTTGGAGGCAGCATGGTTTGATTAGCATTTCCGCA
TCCATGCAAACGAGTCACATATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAA
CTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTA
CTCAGCGATCTATTCTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACT
ACCTAAATGTGATTTTGTGGTTACTAAAATATTCTTACCCTTAAAAGAGCAAGCTAACACAT
TGCTTTAAGCTGATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGAT
TTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCTGTATAGCATCATT
ATTTTGTAGCTTTCTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAAC
TGTATTTTAAATACTTAACCACTAATTTTGAAAATTACAGTGTGATACATAGGAATCATTATTC
AGAATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTGAGA
AAGGACTTGTATGCTGTTTTTCTCCCAATGAAGACTTTTTTGACACTAAACACTTTTTAAAAA
GCTTATCTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCACAGAAAA
TAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAACATGTGACAATTTAGAGATT
CTTTGTTTTATTCTACTGATTAAATATCTGTGGCAAATTACACAGATTATTAAATTTTTTACAA
GAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTACTGTATTTTGTGATTTTGTATTAT
TTCTCAGAAATATGGAAGAAAATAAAATGTGTCAATAAATATTTCTAGAGAGTAA

FIGURE 108

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVVHP
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMT
LKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGCSKQAHQ
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDRREPGTDQM
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 109

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCTCTGATAAAGCCCTACCAGTGCT
 GATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCCTTAAAAAAGTGCTTGAAAGAGAAGGGGACAAAGGAACA
 CCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTCCAGAAGGATGCCTCCATTCTGCTTCTCACCTG
 CCTCTTCATCACAGGCACCTCCGTGTACCCGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGC
 CCTGGAGGAACACTGACCACCAAGTTGGATGAGTCTCAAGGTCCTCTCTATGTGACAACCATGTGAATGGGGAG
 TGGTACCACCTTACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAACCCA
 CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCAGGCTTGTGCCAGCT
 TCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT
 CTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGGTCATTTTATGACATCTGCGACGAGGACTGCCATGG
 CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAACCTGTGCTAGGCCCTGACAGGCAGACATGCTTTG
 ATGAAAATGAATGTGAGCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGT
 GAGTGTGGGGTGGCCGTGTGCTAAGAAATGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA
 TGGTGGCTGCAGCCACTCTTGCCTGGATCTGAGAAAGGCTACCAAGTGTGAATGTCCCCGGGGCTGGTGTGT
 CTGAGGATAACCACTTGCACAGTCCCTGTGTTGTGCAAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG
 CTGGTTGGTGGCCTGGAGCTCTTCTGACCAACACCTCCTGCCGAGGAGTGTCAAACGGCACCATGTCAACAT
 CCTCTTCTCTCAAGACATGTGGTACAGTGGTGCATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGA
 CAGGTCTACCAAGCAGACCCCGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTG
 ACCTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCCACTGGAAT
 CATGAGCCGAAATCATGGGATCTTCCCATTCCTCTGGAGATCTTCAAGGACAATGAGTTTGAAGAGCCTTACC
 GGGAGCTCTGCCACCCCTCAAGCTTCGTGACTCCCTCTACTTTGGCATTGAGCCCGTGGTGCACGTGAGCGGC
 TTGGAAAGCTTGGTGGAGAGCTGCTTTGCCACCCACCTCCAAGATCGACGAGTCTGAAATACTACCTCAT
 CCGGGATGGCTGTGTTTCAGATGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGG
 TCCCTGTCTTCAAGTTTGTGGGCAAGACCACAAGGAAGTGTCTGCACTGCCGGTCTTGTCTGTGGAGTG
 TTGGACGAGCGTTCCTCGCTGTGCCAGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGGAGGACTCAGC
 CGGTCTACAGGGCCAGACGCTAACAGCGGCCCGATCCGCATCGACTGGGAGGACTAGTTTCGTAGCCATACCTC
 GAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC
 TGGGTTTCACTTTCACACTGTGAGTTCAGACTCCAGCACCAACTCACTCTGATTCTGGTCCATTCACTGGGCA
 CAGGTACAGCACTGCTGAACAATGTGGCCTGGTGGGTTTCATCTTTCTAGGGTTGAAAATAAAGTGTCCA
 CCCAGAAAGACACTCACCCATTTCCTCATTTCTTCTTACACTTAAATACCTCGTGTATGGTGAATCAGAC
 CACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAAACCTAGAAAAATTAAACAGTTACTGAAATATGA
 CTTAAATACCCATGACTCCTTAAATATGTAATATAGTTATACCTTGAATTTCAATTCAAATGCAGACTAA
 TTATAGGGAATTTGGAAGTGTATCAATAAACAGTATATAATTT

FIGURE 110

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP
TFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPGGYVYRLTKPSVCFHV
YCGHFYDIDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV
LRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRGLVLSNHTCQVPVLCKSNAIEVNI PRELVGG
LELFLTNTSCRGVSNNGTHVNILFSLKTCGTVVDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT
CEFPRLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEEFYREALPTLKLRLDSLYFGIEPVVHV
SGLESLVESCFATPTSKIDEVLKYILRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV
LVCGLDERSRCAQGCCHRRMRGAGGEDSAGLQGQTLTGGPIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 111

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGG
GCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCT
CCTGCTGCCCTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCCGAAACCCCGTATCCCC
ATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGT
GGTTGTCTCATCAAGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGA
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTC
CCCGAAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCAC
AGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTAGGCAGATGG
GCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAATCACAGAAAACAGCCAG
GAGCTTCGCATGCCGAACCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCACTGTCTTGCTG
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTTGGCAGG
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCA
GCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAG
CTTCCCATCCCTGGCTGTGGCCAAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACA
TCGCCCTCATGAAGCTGCAGTTCCTCACTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCTTT
GATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGAATGGAGGGAA
GATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGTGCAATGCAGACGATGCGT
ACCAGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGT
GACAGTGGTGGGCCCCGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGG
CTGCGGGGGCCCCGAGCACCCCAAGGATATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT
GGAAGGCTGAGCTGTTAATGTCTGCTGCCCTTTGCAGTGTGGGAGCGGCTTCCTTCCTGCCCTGCCACCT
GGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCAT
TCTTGGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGCCCTCGCAGCCCAGAGGCGCCAGAGGAAGTCA
GCAGCCCTAGCTCGGCCACACTTGGTGTCTCCAGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCT
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTACTGAATGGAAGCAGGCTGTCTTGTAAAAGCC
CAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAA
GCCTACTAGAGCAAGAAACCAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT
ACTGTTGTCATTGTTATTACAGCTATGGCCACTATTATTAAGAGCTGTGTAACATCTCTGGCAAAAAAAA
AAAA

FIGURE 112

MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSIASIIIVVVLIKVILDKYYFLCG
QPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN
FTEALAEACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSLHCLACGKSL
KTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL
GSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTPATPLWIIIGWG
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTCCQGDSSGGLMYQS
DQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 113

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGATTA
TAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCACAGGAGT
TGAACCTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC
TGTTTTTTGTTCTCTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACTGTGGCTCT
GGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGTCCCCTCGAAG
CCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCACCTGTCTCACGTCT
GGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGGCTTTCAAGGTGGGC
CTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATTTCATAGGCGATGGCTCCCCTGCCCC
AGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGGGCGGTGGACACCTGTCTCA
GAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTTCATGTCTGCACATCACCTG
ATCCATGGGCTAATCTGAACCTCTGTCCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC
CAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGACTTGCATTCTCTGGAACATGAGG
GAACGCCGAGGAAAGCAAAGTGGCAGGGAAGGAACCTGTGCCAAATTATGGGTCAGAAAAGATG
GAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGCATTCACTGGACATGTGGGGGAAGGGCTG
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCCGAT
CCACGTACCAGCTGCTGAAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAA
TCTGCGATCACCAGCCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCC
CTCCTTCCCTCTGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG
GGCTAATGGCTCAGTGTTGGCCCAGGAGGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCT
GTGCGAACACGGAATGCCCTCAGTAAGCACAGGCTGCAAAATCCCAGGCAAAGGACTGTGTGG
CTCAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGTTT
CAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCA
AACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACAT
TTTGGGAGGCCGAGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGG
TGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATC
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACA
GGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTA
TGGTTATTTGTAA

FIGURE 114

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTASPC
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FIGURE 115

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA
AGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
ATATGTAAATCACTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCTAATTGTCCT
GTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT
TCTACAGCAATGGAGAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAAGTGAATA
TTCAGAAGCGGAAATGGCACTGATGAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGG
CATCTACTTCGTGGGTCTTCAAAATGTTTTATCAAACTCAGATTAAAGTGATTCCTGAATTTT
CTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACCTTCTTTGAACAGTCAGTG
ATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCCTGGA
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAG
ACTTTGAGGAGGAGGAGAAGATCTTCACTTTCTGCCAACGAAAAAAGGGATTGAACAAAAT
GAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGA
AGAACTTCCAATAAATGACTATACTGAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAG
GTTATTGTGTATTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCTCTGTGAACCTTTACTA
GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCCTTG
TAACTGGTGGGTGGCCCGCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAAAC
TGCTGGCAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCT
GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATCCTCTCTTCATGTTCTAATAAATCTCTACA
TTATCACCAAAAAAAAAAAAAAAAAA

FIGURE 116

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAYDME
HTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIIYFVGLQKCFIKTQIKVIP
EFSEPEEEIDENEEITTTTFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWINPTLISVSE
LQDFEEEGEDLHFPANEKKGIEQNEQWVPQVKVEKTRHARQASEEELPINDYTENGIEFDPMLD
ERGYCCIIYCRRGNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWVARMLGRV

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-
242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 117

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGCAGGCGGCA
GGCGGGCGGCCAGGATC**ATG**TCCACCAACCACATGCCAAGTGGTGGCGTTCTCTGTCCATCCTGGGGCT
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCC
TATTTACCATCCTGGGACTTCCAGCCATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCCT
GGGTGCCATTTGGCTCCTGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG
CCAAAGCCAAACATGACACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTG
TCTGTGTTTGCCAAACATGCTGGTGACTAAGTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTGG
GATGGTGACACTGTTTACAGCAGGTACACATTTGGTGGCGCTCTGTTCTGGGCTGGGTGCTGGAGGCC
TCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGCGCTGGCACCAGAAGAAACCAACTACAAA
GCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTT
TGGGTCCAACACCAAAAACAAGAAGATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATC
CTTCCAAGCACGACTATGTG**TAAT**GTCTTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCA
CCCAAAAACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAGTTAGAAAAGCCT
CGATTTCACTCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCACCATAAAACA
GCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTCTTTTTTAAATATAACT
TTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAGACTCCCCCTC
TTCTCCTAGTCAATAAACCATTGATGATCTATTTCCAGCTTATCCCCAAGAAAACCTTTTGAAGGAAA
GAGTAGACCCAAAGATGTTATTTCTGCTGTTTGAATTTGTCTCCCCACCCCAACTTGGCTAGTAATAA
ACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTT
ACACTGTGATCTTAAAAGTTACCAAACCAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTG
TTGACATCTTCTTATTACAGCAACACCATTTAGGAGTTTCTGAGCTCTCCACTGGAGTCTCTTCTGT
CGCGGGTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTAATTTAAGTCCATAATATAGTTAA
AATAAATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAGAAG
GAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCC
ATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGT
TCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAATCAGCCAGTCA
TGGTGGCATACACCTGTAGTCCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGT
TGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAA
AATAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

FIGURE 118

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTECRP
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSI FALKCIRIGSMEDSAKANMTLTSGIMFIVSGL
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGGVMMCIA
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYPSKHDY
V

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 119

GGAAAACTGTCTCTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCGGAGTCC
AGCTGGCTAAAACATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGGCTGTTCTTG
GTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGAGTGTGGCCTTCATT
GAAAACAACATCGTGGTTTTTGAACCTTCTGGGAAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA
CATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGGCTCTTCTCCGGACCTACAGGCAGCCAGAG
GACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCTTTCATGATGGCCATCCTTGGCATGAAATGC
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCAT
CATCACGGGCATGGTGGTGTCTATCCCTGTGAGCTGGGTGCAATGCCATCATCAGAGATTTCTATA
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTTGAGAAGCTCTCTACTTAGGATGGACCACGGCA
CTGGTGTGATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGCAACGAAAAGAGCAGTAGCTA
CAGATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTATCACACCGAAAGAAGTCACCGAGCG
TCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATG
ACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGCCT
AATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATCTATAAGCTATTTACGAGAATGAGATA
TTAAACCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGGTTCAAGCATCTA
CTCTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTTACTACTGTAATTTCTCC
ACGACATAGCATTATGTACATAGATGAGTGTAACTTTATATCTCACATAGAGACATGCTTATATGGT
TTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAA
ATCATGGATAGGGTTGAAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCCTCCA
TTTATAATGAAGATTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATAT
GCTGTTTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTT
CTTGTGTATTAAATTAACATTTTAAAAACGCAGATATTTGTCAAGGGGCTTTGCATTCAAACCTGCTT
TTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTG
AAAATATTTTTGTTTTGTATTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGAT
ATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAGAGCAGAAAAATA
TGTCTTGGTTTTTCATTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTCACCT
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTGTCTGTGAAAAATAAATTCCTTCTTGTA
CCATTTCTGTTTAGTTTTACTAAAATCTGTAATACTGTATTTTCTGTTTATTCCAAATTTGATGAA
ACTGACAATCCAATTTGAAAGTTTGTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTT
TATACATTTATATTAATAAATGTACATTTTCTAATT

FIGURE 120

MATHALEIAGLFLGGVGMVGTVAVTVMPPQWRVSAFIENNIIVVFENFWEGLWMNCVRQANIRMQCK
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIFIITG
MVLVLPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCNEKSSSY
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 121

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGGAG
CCAGACGCTGACCACGTTCTCTCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCC
GGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCGCAGCGGCTCCGCGGCCTCCTGCTGCTCC
TGCTGCTGCAGCTGCCCGCGCGCTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAAAGGCGCAG
CTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC
TGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCGGGTACACCTGGGATCCCAGGTCGGGATG
GATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAGCTTTGAGGAGTCCTGGACACCCAACCTAC
AAGCAGTGTTTCATGGAGTTTCATTGAATTATGGCATAGATCTTGGGAAAATTGCGGAGTGATACATT
TACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTGTTCAGTGGCTCACTTCGGCTAAAATGCA
GAAATGCATGCTGTCAGCGTTGGTATTTTCACATTCAATGGAGCTGAATGTTTCAGGACCTCTTCCC
ATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAATATTCATCG
CACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGTGGATTAGTGGATGTTGCTATCTGGG
TTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATC
ATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCC
TTGGAATGGTTCACCTAAATGACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTTACAGACCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTG
CTTCAATCAAAGTGGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATT
CTCTCAACCTATAATTTGGAATATTGTTGTGGTCTTTGTTTTTCTCTTAGTATAGCATTTTTA
AAAAATATAAAGCTACCAATCTTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGT
TAAATAAAAATTATTTCCAACA

FIGURE 122

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAQVPGR
DGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTK
MRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPENSTINIHRIS
SVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 123

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCTGAA
CTGGGTGCTCATCACGGGAACCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCCCCAA
ATTGCTTGAAGAATACATCATGTTTTTCGATAAGAAGAAATGTAGGATCCAGTTTTTTTTTA
ACCGCCCCCTCCCCACCCCCCAAAAAAAGCTGTAAGATGCAAAAACGTAATATCCATGAAGATCC
TATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTTGTTCTTGGAG
TGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCAAGGGTCCAATTTT
TCTTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTGACAGGGGCTGTGATGCAACTG
GCCCCAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAAAGGATGGGTTTCAATG
TAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCACTGTCTTACTGACAATG
CTTCTCTGCGGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAAGGCAAAATGGTATATTGTGA
ATCTCAGAAATTACAGGAGATACCCTCAAGTATATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCT
ATAACAGCCTTCAAAAACCTTAAGTATAATCAATTTAAAGGGCTCAACCAGCTCACCTGGCTATAC
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTTAATGGAATACGCAGACTCAAAGA
GCTGATTCTTAGTTCCAATAGAATCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAAT
TACGGAACCTTGGATCTGTCTTATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTG
CGGAAGCTGCTGAGTTTACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA
AGACTGCCGCAACCTGGAACCTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATG
TCTTTGCTGGCATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTTCCAAGCTCAAC
CTGGCCCTTTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAATAAAATCAGTGT
CATAGGACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGA
TCGAAGCTTTCACTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGAT
TCCAACAAGCTCACATTTATTGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAG
TCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTTGTAAGCTGGCTGAAAAGTT
TTAAAGGCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAGAGCTGCAAGGAGTAAATGTG
ATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAG
GGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAAACCCCTT
TGCCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGCTGACGCCGAGCACATCTCT
TTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCCTGCTGGTTAT
CTACGTGTGATGGAAGCGGTACCCTGCGAGCATGAAGCAGCTGCAGCAGCGCTCCCTCATGCGAA
GGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAATGACTCCAGCACCCAGGAATTTATGTA
GATTATAAACCACCAACACGGAGACCGAGATGCTGCTGAATGGGACGGGACCTGCACCTA
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCATTTGTGATAAAAAGAGCTCTTAAAGCT
GGGAAATAAGTGGTGCTTTATTGAAGTCTGGTGACTATCAAGGGAACGCGATGCCCCCCTCCCC
TTCCCTCTCCCTCTCACTTTGGTGGCAAGATCCTTCCTTGTCGGTTTTAGTGCAATTCATAATACT
GGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTT
GAACTCCGGTTTAATATAATACCTATTGTATAAGACCTTTTACTGATTCCATTAATGTGCGATTT
GTTTTAAGATAAACTTCTTTTCATAGGTAAAAA

FIGURE 124

MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEIPSSISAGCLG
LSLRYNLSQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYFLNNTFR
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELLDLGYNRIRS
LARNVFAGMIRLKEHLEHNQFSKLNLFPRLVSLQNLQWKNISVIGQTMSWTWSSLQRLDL
SGNEIEAFSGPSVFCVFNQLRLNLD SNKLTFIGQEILD SWISLNDISLAGNIWECSRNICSLVN
WLKSFKGLRENTIICASPKELGQVNVDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRPKHE
SKPPLPPTVGATEPGPETDADA EHFH KIIAGSVALFLSVLVILLVIYVSWKRYPASMKQLQQR
SLMRHRHKKRQSLKQMPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

Important features of the protein:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 125

CCGTTATCGTCTTGCGCTACTGCTGAATGTCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCGCTG
ACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGCCGAGCT
AGCAACCTTTCCCTGGATCTCACAAAACCTCGACTCCAAATGCAAGGAGAAGCAGCTCTTGCTC
GGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACAGCCCTAGGGATC
ATTGAAGAGGAAGGCTTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCATTTACAGACACGTAGT
GTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTTGGCAAAGTGAAG
ATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCCAGTTT
TTAGCCAATCCAACGACCTAGTGAAGGTTTCAGATGCAAATGGAAGGAAAAGGAAACTGGAAGG
AAAACCATTCGATTTTCGTGGTGACATCATGCATTTGCAAAAATCTTAGCTGAAGGAGGAATAC
GAGGGCTTTGGGCAGGCTGGGTACCCAATATACAAAGAGCAGCACTGGTGAATATGGGAGATTTA
ACCACCTTATGATACAGTGAAACACTACTTGGTATTGAATACACCACTTGAGGACAATATCATGAC
TCACGGTTTATCAAGTTTATGTTCTGGACTGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCA
TCAAAGCAGAATAATGAATCAACCACGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCG
ACTGACTGCTTGATTTCAGGCTGTTCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACC
ATCTTGCTGAGAATGACCCCTTGGTCAATGGTGTCTGGCTTACTTATGAAAAATCAGAGAGA
TGAGTGGAGTCAGTCCATTTTAA

FIGURE 126

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNP
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLEVVFGKSEDEHYPLWKS
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRRKLEKPLRFRGVHHAFAKILAEGGIRGLWAGWVP
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSRIMNP
RDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

FIGURE 127

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGCGGCGAGAGCGGCCGGCGTCAGCTCCTCGAC
CCCCGTGTGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGCATGG
AGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCTCGGGGGGCATCGGCGCGGCCGTGGCC
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAACATCGAGGA
GCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGACTTTGATCCCCACAGATGTGACCTAT
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATC
TGCATCAACAATGCTGGCTTGGCCCGGCTGACACCTGCTCTCAGGCAGCACCAGTGGTTGGAA
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGA
AGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTTA
CCCCGTGTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGGACT
GAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTGGTGG
AGACACAATTGCGCTTCAAACCTCCACGACAAGGACCCTGAGAAGGCAGCTGCCACCTATGAGCAA
ATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCAGCACCCCGCACA
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTACTGTGGGAGCTCC
TCCTTCCCTCCCCACCCTTCATGGCTTGCTCTGCTCTGGATTTAGGTGTTGATTTCTGGAT
CACGGGATACCACTTCCTGTCCACACCCCGACCAGGGGCTAGAAAATTTGTTTGAGATTTTATA
TCATCTTGTCAAATTGCTTCAGTTGTAAATGTGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCC
TAATTGTTTTACTTGTTAACTTGTTCTTGTGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTG
TCTTCCCTTTGACATGGGAAAGGAGTTGTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTG
TGGCTCAGGGCTGGGGTGGCAGAGGGAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCC
AGACTTCCTCCTCTGCCTGCCCCACTGCACCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCC
AGCCCAGTCTTGGCTTCTTGTCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAG
CAGAACACCAGGGCCTGGCCAGTGGATTTCATGGTGATCATTAAAAAAGAAAAATCGCAACCAA
AAAAAAAAA

FIGURE 128

MARPGMERWRDRLALVTGASGGIGAARALVQQGLKVVGCAITVGNIEELAAECKSAGYPGTLI
PYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDLLSGSTSGWKDMFNVNVLALSICTR
EAYQSMKERNVDDGHIININSMGHRVLPVSVTHFYATKYAVTALTEGLRQELREAQTHIRATC
ISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 129

AAC TTCTAC ATGGGCCTCCTGCTGCTGGTGTCTCTCCTCAGCCTCCTGCCGGTGGCCTACACCAT
CATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGGGAGC
ACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTGGTTTCATGC
CAGCCTGTAAAAGGCCATGGAAC TTTGGGTGAATCACC GATGCCATTTAAGAGGGTTTTCTGCCA
GGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCA TTTCAGTAGCCACCAGCCACCTGTGG
CCGTTGAGTGCTTGAAAT TCAGGAACTGAGAAAATTAATTTCTCATGTATTTTCTCATTATTTA
TTAATTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGGATACATGTATACAA
TATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACATTTATTTTTTATTCTTT
TTAGACAGAGTCTCACTCTGTCA CCGAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAAC
CTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCAT
GCACCACAATGCCCAACTAATTTTTGTATTTT TAGTAGAGACGGGGTTTTGCCATGTTGCCAGG
CTGGCCTTGAAC TCTGGCCTCAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTATGATTACA
GGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGGAAC TTTGAAATTAT
ACAATGAATTATTGTTAACTGT CATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT
ATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCTCCTCTCTATCCTTCCC
AACCTCTGATCACCTCATCTACTCTCTACCTCCATGAGATCCACTTTTTTAGCTCCCACATGTG
AGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTCCTG
TTCCATCCATGTGCTGCAAAATGACAGGATTTGTTCTTAATTTCAATTAAATAAACCACACATG
GCAAAAA

FIGURE 130

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQPV
KGGHTLGESPMPEKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 131

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAGCCTGGAGC
 ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCTG
 TCCATCTGTGTGCTGCGATGCGGGTTTCATTTACTGTAATGATGCTTTCTGACATCCATTCCAACAG
 GAATACCAGAGGATGCTACAACCTCTTACCTTCAGAACAACCAAATAAATAATGCTGGGATTCCCTTCAGAT
 TTGAAAACTTGCTGAAAGTAGAAGAATATACCTATACCACAACAGTTTAGATGAATTTCTACCAACCT
 CCCAAAGTATGTAAGAGATTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAA
 AATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTGCTGCTCTGCAGTTAGCATAGAAGAGGGAGCA
 TTCGAGAGCAGCAACTATCTCCGACTGCTTTTCTGCTCCCGTAATCACCTTAGCACAAATCCCTGGGGTTT
 GCCCAGGACTATAGAAGAACTACGCTTGATGATAATCGCATATCCACTATTTTCATCACCATCTCTTCAAG
 GTCCTACTAGTCTAAAACGCCTGGTTCTAGATGGAACCTGTTGAACAATCATGGTTTAGGTGACAAAGTT
 TTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCAGAAATCCCTGACTGCTGCACCAGTAAACCT
 TCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATAACCACATCAATCGGGTGGCCCCAAATGCTTTTT
 CTTATCTAAGGCAGCTCTATCGACTGGATATGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTT
 GATGATTTGGACAATATAACACAACCTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATG
 GGTACGTGACTGGTTACAATCACTACCTGTGAAGGTCAACGTGCGTGGGTCATGTGCCAAGCCCCAGAAA
 AGGTTCTGTTGGATGGCTATTAAGGATCTCAATGCAGAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC
 ACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAGTCCAGTGAC
 CAAACAGCCAGATATTAGAAGCCCCAAGCTCACTAAGGATCAACAACCAACAGGGAGTCCCTCAAGAAAAA
 CAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCATATCTCTTGGAACCTTGCTCTACCTATG
 ACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATAGCCCGGCATTTGGATCTATAACAGAAACAATTGT
 AACAGGGGAACGAGTGAGTACTTGGTCACAGCCCTGGAGCCTGATTCACCTATAAAGTATGCATGGTTC
 CCATGGAAACAGCAACCTCTACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTT
 CGAATGTACAACCTACAACCACCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAACCCCAATTTACC
 TTTGGCTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGTATG
 TTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT
 GCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTTCTTTTCAGATGTTACCAAT
 AAGCAATGAACCATCTCGAAGGAGGAGTTTGTAAATACACCATATTTCTCCTAATGGAATGAATCTGT
 ACAAACAATCACAGTGAAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC
 TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTTTGGGTTTTTAAACCTAAGGGAGGTGATG
 GT

FIGURE 132

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTLYL
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL
EELHLDNDSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRISTISSPSL
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAFPVNLPGTNLRKLYLQDNHIN
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDLDNITQLILRNNPWCYCGCKMKWVRDWLQSLPV
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQGQWPAPVTKQPD
IKNPKLTKDQQTGTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWLKLGHSPAFGSITET
IVTGERSEYLVTALEPDSYKVCMPMETS NLYLFD ETPVCIETETAPLRMYNPTTTLNREQEKE
PYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRRKDDYAEAGTKKDNS
ILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSESSSNRSYRDSGIPDSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 133

CCGTCATCCCCCTGCAGCCACCCCTCCCAGAGTCCTTTGCCAGGCCACCCAGGCTTCTTGGA
 GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG
 TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGTGAGCGTGTGACCAGCAGTGAGCAGAG
 GCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACCCTGTGGT
 CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCTGATCCTGTCT
 GCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT
 GGGGGTCCGAGTGTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCTGC
 TGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC
 CTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCAGCTGACCCCTCCAGCCCGG
 GTTTTGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTTGGTGTACCCACGTTCCGGC
 CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGTGCAGCTGCTGGGAACCGGGACG
 GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCCGGCTGCTC
 AGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTCTGGGCCAGAATGAGGGGATGCACACAGG
 GACCACTCCAACAGAGCCAGGACTATATCAACCTCTTCTGCGCCAACATGATGGACTTGAACCGC
 AGAGCTGAGGCCATCGGATACGCCTACCCTACCGGGACATCTTCATGGAACATCATGTTCTG
 TGAATGGGCGGCTTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA
 AACAGCAGGAAGGATGCTTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA
 TATCAGCAGCATTTTTCGAGGAGAGTGAAGAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGT
 TGCTCAGGCTGGAGTACAGTGGCGCAATCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAGC
 AATTCTCTTGCCCTCATCTCCCGAGTAGCTGGGACTACAGGAGCGTGCCACCATACCTGGCTAAT
 TTTTATATTTTTTAGTAGAGACAGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGAT
 CTCAAGAGATCCGCCACCTCAGGCTCCCAAAGTGTGGGATTATTAGGTGTGAGCCACCGTGTCTG
 GCTGAAAAGCACTTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTC
 ATGGGGGCTCTCTCCCTAGATGGCTGCTCTCCACAAACACAGCCACAGCAGTGGCAGCCCTGG
 GTGGCTTCTATACATCTTGGCAGAAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCG
 CCACCACCAAGCAGCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCC
 TTTAGTCCTCATCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG
 ATAAGCAAAGCCACCCGACACCCAATCTTGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG
 GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAA

FIGURE 134

MSARGRWEGGRRACRGSGLLARAQGAERTVSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPGLD
TAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPLSLRV
GMLGEKLEAAIQRSLSHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD
YINLFCANMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSQKQEGCFG
EPDAEDEELSKAIQYQQHFSSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFKQFSCILIP
SSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 135

GGTCTGAGTGCAGAGCTGCTGTCAATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGCTG
CTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGCTGCTGCTGAGGGATCGGGAGG
GAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGGTGAAGC
CTCAGGACTGGATCTCGGCGGCCCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTTCCCTTAAG
ACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGAAGTTGTATCTCC
AGCTTACAGATTTGATCCCGTTTCGAGTGGATATCACTTCGAAAGGAAAAATGAGAGCAAGATATG
TGAATTACATCAAAACATCAGAGGTTGTGAGACTGCCCTATCCTCTCCAAATGAAATCTTCAGGT
CCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTCTAATGAACCCAATGGT
TATGATGATGGTTCTTCTTTATTGATATTTGTGCTTCTGCCTAAAGTGGTCAACACAAGTGATC
CTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATCCAACCATGAGTTGCCTGAT
GTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAATCATCTGGCAAATCTAGCAGCGGCAGCAG
TAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTTCAC
AAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAAACCGTGTGAAGCAACTACTATAAACTT
GAGTCATCCCGACGTTGATCTCTTACAACCTGTGTATGTT
AACTTTTGTAGCACATGTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGTAT
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAATTAT
ATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAA

FIGURE 136

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEKSGSGVGIGDRFKIEGRAVVPGVKPDWISAA
RVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSAPYRFDVVRVDITSKGKMRARYVNYIKTSE
VVRLLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLIFVLLPKVVNTSDPDMRREME
QSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 137

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA
CCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAACAA
GTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCTGCTGTTCCAGGC
CTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACGACCTGTGC
CACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTACGGGAGGCTTGGCAGT
TTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGTCTTGCCTTCAGC
CTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAGACACTCAATTTGGG
AAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTCTGAGATACGGGGCAGTG
TGCAAGCCAAAGATGGAACATTGACATCAGAATCTTAAGGAGGACTGAGTCTTTGCAAGACACA
AAGCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTCTATCTGGACAGGGTATTTAA
AAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGCAGCCTCGCCAATTCCTTTCTTA
CCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACATGCCATGTGGGGAGGAAGCAATG
AAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGC
TTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAGGAGACAGAAATAGGAGGAAAGTGATGCTG
CTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAA
ACCACCATCTCTTTACTGTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTATGCATTACTTG
CTTCCTTGCATGATTGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTT
TGTAATATCTTCTGCTATTGATATATTTATTAGTTAATATATTTATTTATTTTGGCTATTTA
ATGTATTTATTTTACTTGGACATGAACTTTAAAAAATTCACAGATTATATTATAACCTG
ACTAGAGCAGGTGATGTATTTTATACAGTAAAAAATAACCTTGTAATCTAGAAGAGTGG
CTAGGGGGGTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGAT
ATTTGAAATTGAACCAATGACTACTTAGGATGGTTGTGGAATAAGTTTGTGATGGAATTGCAC
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATTAATTGTGTATCTTCCAG
CCAGGAATCCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTCTTTCATACCAAAAAA
AAAAA

FIGURE 138

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGATTTCATNSHSDSELRPEIF
SSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG
FSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHYTLRKIS
SLANSFLTIIKDLRLSHAHTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET
E

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 139

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCCGGTCCGCATCCAGCC
 TAGCGTGTCCACGATCGCGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCGAGGTGC
 TAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCGGCTCCCGTTCGTTCTCTGCCAGAGCGGAA
 CACGGAGCGGAGCCCCCAGCGCCCCGAACCTCGGCTGGAGCCAGTTCTAACTGGACCACGCTGCC
 ACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAGATGATTTTGTGTTTG
 GGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTACCTTGTGGAAAAAGGAGCATCTCACAGT
 TTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAATCAAGGCATTGATGACGGGGAG
 CCTTCCTGGCTTTGTGACGTCATCAGGAACCTCAATTCTCCTGCACTGCTGGAAGACAGTGTGA
 TAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTTTATGGAGATGAAACCTGGGTAAATTA
 TTCCCAAAGCATTTTGTGGAATATGATGGAACAACCTCATTTTTTCGTGTGAGATTACACAGAGGT
 GGATAATAATGTCACGAGGCATTTGGATAAAGTATTAAAAAGAGGAGATTGGGACATATTAATCC
 TCCACTACCTGGGGCTGGACCACATTGGCCACATTTCAGGGCCCAACAGCCCCCTGATTGGGCAG
 AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGA
 GACGCCTTTACCCAATTTGCTGGTTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACG
 GGGCTCTCCACCGAGGAGGTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAGGAAA
 CCCGGTGATATCCGACATCCAAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCGATAGC
 ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGAC
 CAATGAGAGAGCAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAACTGTTGCAAGAG
 AATGTGCCGTATATGAAAAGATCCTGGGTTTGTAGCAGTTTAAATGTGAGAAAGATTGCATGG
 GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCCTATTCAACCTGGGCTCCAAGG
 TTCTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCCTGAGTGCACAAGTGGCCCCAG
 TTCTCACCTGCTCCTGCTCAGCGTCCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCCA
 CTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTGTTGATCCTGGTTCTTTTCGGCCGTTACGT
 CATTTGTGTGACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGECCTCTCGTGGCTGGCGGAGGCT
 GCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGTGTCAGTGCCTTGGAC
 AGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCAGGCCTCTGGGTGTCCCGACACAGGTG
 TTCACATCTGTGCTGTGTCAGGTGAGTGCCTCAGTTCTTGGAAAGCTAGGTTCTGCGACTGTTAC
 CAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCCCCAGCTGAGGGGGTGTGTGAA
 TCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGAGGGAAGAAGAGACAATCGGCCTGGA
 CACTCAGGAGGGTCAAAAGGAGACTTGGTCGCACCACTCATCCTGCCACCCCAAGATGCATCCT
 GCCTCATCAGGTCCAGATTTCTTTCCAAGCGGACGTTTTCTGTTGGAATCTTAGTCCCTGGCC
 TCGGACACCTTATTGTTAGCTGGGGAGTGGTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCAC
 ACTCAGATCCACAGAGCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCC
 ACCCCAACCTGACAGCCCTCATCCCTCTTGGCTTGAGCCGTGAGAGGCCCTGTGCTGAGTGT
 CTGACCGAGACACTCACAGCTTTGTATCAGGGCACAGGCTTCTCGGAGCCAGGATGATCTGTG
 CCACGCTTGCACCTCGGGCCCATCTGGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAG
 CTGCACACAGTATGTAGTTACCAAAAGAATAAACGGCAATAATTGAGAAAAAAA

FIGURE 140

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEGAEPPAPEPSAGASSNWTTLPPPLF
SKVVIVLIDALRDDFVFGSKGVKFMPTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF
VDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSTFFVSDYTEVDNNV
TRHLDKVLKRGDWDILILHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

Important features of the protein:

Signal peptide:

amino acids 1-34

Transmembrane domain:

amino acids 58-76

N-glycosylation sites.

amino acids 56-60, 194-198

N-myristoylation sites.

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,
275-281, 278-284

Amidation site.

amino acids 154-158

Cell attachment sequence.

amino acids 205-208

FIGURE 141

GGCACGAGGCAAGCCTTCCAGGTTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACA
GAAAGTTACTAGTGCCCTAAAGCTGGCGCTGGCACTGATGTTACTGCTGCTGTTGGAGTACAACT
TCCCTATAGAAAACAAC TGCCAGCACCTTAAGACCACTCACACCTTCAGAGTGAAGAACTTAAAC
CCGAAGAAATTCAGCATT CATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCAT
AGCAGTTCAGATAAAAACTACATACGCCCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCT
CAGCCTCTGCGGAGAAAGGAAGTCCGATTCTCCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTAC
TGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCT
GGCTGCCCCAAAAGGAATCAGCACGCCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGA
ACATGCTGGAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCT
GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTGAATTTTCATTTCAACCAGTTTGCAA
AGCTGAAATGAGCCCCAGTGAGGTCAGCGATTAGGAAACTGCCCCATTGAACGCCTTCCTCGCTA
ATTTGAACTAATTGTATAAAAACACCAAACCTGCTCACT

FIGURE 142

MLLLLLLEYNFPIENNCQHLKTTHTFRVKNLNPKKFSIHDQDHKVLVLDSGNLIAVPDKNYIRPEI
FFALASSLSSASAEKGSPELLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 33-36

N-myristoylation site.
amino acids 50-55, 87-92

Interleukin-1
amino acids 37-182

FIGURE 143

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTTAA
TCCAGGATCCTGTCTTCTGTCTGTAGGAGTGCTGTTGCCAGTGTGGGGTGAGACAAGTTTG
TCCCACAGGGCTGTCTGAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACCTGTGGG
CACGGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCATGCTGGGCCTGCCGTGG
AAGGGAGGTCTGTCTGGGCGCTGCTGCTGCTTCTCTTAGGGCTCCCAGATCCTGCTGATCTATGC
CTGGCATTTCACGAGCAAAGGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA
CAGTGGAGTTTGTCTGTCCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG
CACATCTTGAATTCCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT
GGGGAGAAGTAGGTGTGGGAAATTTGAAGACGACATTGACAACCTGCCATTTCCAAGAAAGCACAG
AGCTGAACAATACTTTCACCTGCTTCTTCACCATCAGCACCAGGCCCTGGATGACTCAGTTCAGC
CTCCTGAACAAGACCTGCTTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGTCATGT
GCTGCTCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTTCAGTGGCTGAGCAGCT
TTGGACTTGTTTGTATCCTATTTTGCATGTGTTTGAATCTCAGATCAGTGTTTTAGAAAATCC
ACACATCTTGAGCCTAATCATGTAGTGTAGATCATTAACATCAGCATTTTAAGAAAAAAAAAA
AA

FIGURE 144

MLGLPWKGGLSWALLLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP
WMTQFSLLNKTCLEGFH

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 117-121, 139-143

N-myristoylation site.

amino acids 9-15

FIGURE 145

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGAAG
CACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGGTCCA
GACGAGGGGCATCAAGCACAGAATCAAGTGGAAACCGGAAGGCCCTGCCAGCACTGCCAGATCA
CTGAGGCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGCTCGACATT
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCGATGGCATCCA
CTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCTGCATCAATGCCA
CCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGGTTGGAGAGGGGCGCAGGACT
TCGGGTCAACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGATCTGGCTCATGGTGAAT
AAAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAATCCTGGCAAGTGACCCAGCT
CTTCTCCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGGCGATGCACTCGCACTGCAAA
TGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTCTGATAGATGGGGACTGTGGCTTCT
CCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGAT
GAGAAGAACACATCAGGCACCTGCGCCACCTGCTTCACAGTACTCCCAACAACCTCTTAGAGGTAG
GTGTATTCCCGTTTTACAGATAAGGAACTGAGGCCCAGAGAGCTGAAGTACTGCACCCAGCATC
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGCTTGTCTAACCCAGGTTTTCTGCTCT
GTCCAATTCCAGAGCTGTCTGGTGATCACTTTATGTCTCACAGGGACCCACATCCAACATGTAT
CTCTAATGAAATTGTGAAAGCTCCATGTTTAGAAATAAATGAAAACACCTGA

FIGURE 146

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHKRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ
VLWRLVQELCSLKHCFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 147

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCATT
CCTGATGATTATAGACTCAAAGAAAACTATGTTTCAGAAGCTCTCTTCTCTTCTGGCCTCCTCT
CTGTCTTCTTCCCTCTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG
AAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTTTGAAATTT
CAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCATGATGCTGAGG
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FIGURE 148

MFRSSLLFWPPLCLLSLFLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE
GLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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FIGURE 149

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCCCTACCTGGAGACTTGAC
TCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTGAGAGATCCTGCAGCGCCCACTCC
CGGCCCCCTCTCCCGCCCCACCCACCCCTCCTGGCTCTTCTGTTTTTACTCCTCCTTTTCATTCTATA
ACAAAAGCTACAGCTCCAGGAGCCAGCGCGGGCTGTGACCCAAGCCGAGCGTGGAAGAATGGGGTT
CCTCGGGACCGGCACTTGGATTCTGGTGTAGTGCTCCCGATTCAAGCTTTCCCCAACCTGGAGGAA
GCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAA
GCAGAAGAAGACAAGATTAAAAAACATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATCTTT
TGTTGATAACTTGAACCTGCTAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTA
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGAAGATGTTGATTCAACCAAGAATCGAAAAGT
ATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCA
TCACTAGACGGGACTCCTTTAACCCTGAAGACATTGTCCATAAATCGCTGCCAGGATTTATGAAG
AAAATGACAGAGCCGTGTTTGACAAGATTGTTCTAACTACTTAATCTCGGCCTTATCACAGAAAGC
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAAGCCAACAA
TTATGAGGAGGATCCCAATAAGCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG
TGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGGAGAAAACGATGAAACAGTATCTAACACA
TTAACCTTGACAAATGGCTTGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTTGAGGAACTCCA
ATATTTCCCAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAAGAAGCAAAAGAGAAAGAAA
CACTGATTACTATCATGAAAACACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCT
CCAGAAGAAGGTGTTTCTACCTTGAAAACCTGGATGAAATGATTGCTCTTCAGACCAAAAACAAGCT
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTTTCCAGCACCATCAGAGAAGAGTCATGAAGAAA
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAAAA
GATGATAACTCCAACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTATTTGGAAGC
CATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAGATTATGACCTTT
CAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATCCTTGACAAGGAA
GAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAATGGCAAAAGATCCAGGAGTCTTTCAA
CTGTTTCAGAAAACATAATATAGCTTAAACACTTCTAATCTGTGATTAAATTTTTTGACCCAAGG
GTTATTAGAAAGTCTGAATTTACAGTAGTTAACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCC
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAGAAAAAAGAAAAA

FIGURE 150

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENKPG
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK
FQDDPDGLHQDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMAAIQDGLAKGENDETVSNTLTLTNGLE
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISP EEGV
SYLENLDEMIALQTKNKLEKNATDNISKLFAPSEKSHEETDSTKEEAAKMEKEYGSLKDKSTKDD
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDL SKMRDFINKQADAYVEKGILDK
EEAEAIKRIYSSL

N-glycosylation sites:

amino acids 68-71, 346-349, 350-353

Casein kinase II phosphorylation site:

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-
341, 369-372, 382-385, 386-389, 387-390

N-myristoylation sites:

amino acids 143-148, 239-244

FIGURE 151

CGGCTCGAGGCTCCCGCCAGGAGAAAGGAACATTCTGAGGGGAGTCTACACCCGTGTGGAGCTCAA
GATGGTCCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC
ATAATAACCAGCTTCTAGCTGGAGGGCTGCATGCAGGAAGGTCATTAAAGGTGAAGAGATCAGC
GTGGTCCCCAATCGGTGGCTGGATGCCAGCCTGTCCCCGTCATCCTGGGTGTCCAGGGTGGAAG
CCAGTGCCTGTCATGTGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG
AGCTCTATCTTGGTGCCAAGGAATCCAAGAGCTTCACCTTCTACCGGCGGGACATGGGGCTCACC
TCCAGCTTCGAGTCGGCTGCCTACCCGGGCTGGTTCTGTGTCACGGTGCCTGAAGCCGATCAGCC
TGTCAAGCTCACCCAGCTTCCCGAGAATGGTGGCTGGAATGCCCCATCACAGACTTCTACTTCC
AGCAGTGTGACTAGGGCAACGTGCCCCCAGAACTCCCTGGGCAGAGCCAGCTCGGGTGAGGGGT
GAGTGGAGGAGACCCATGGCGGACAATCAGTCTCTCTGCTCTCAGGACCCACGCTGACTTAG
TGGGCACCTGACCACCTTGTCTCTGTTTCCAGTTTGATAAATTCTGAGATTTGGAGCTCAGT
CCACGGTCTCCCCACTGGATGGTGTCTACTGCTGTGGAACCTTGTA AAAACCATGTGGGGTAAA
CTGGGAATAACATGAAAAGATTTCTGTGGGGGTGGGGTGGGGGAGTGGTGGGAATCATTCTGCT
TAATGGTAACAGCAAGTGTACCCCTGAGCCCCGAGGCCAACCCATCCCCAGTTGAGCCTTATA
GGGTCACTAGCTCTCCACATGAAGTCTGTCACTCACCCTGTGCAGGAGAGGGAGGTGGTCATA
GAGTCAGGGATCTATGGCCCTTGGCCAGCCCCACCCCTTCCCTTTAATCCTGCCACTGTCATA
TGCTACCTTTCCATCTCTTCCCTCATCTCTGTTGTGGGCATGAGGAGGTGGTGTGTCAGAA
GAAATGGCTCGAGCTCAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTCTTTAAAAACCCAA
GATACAATCAAAATCCAGATGTGGTCTCTATTCCCATGAAAAGTGTCTGATGACATATTGAGA
AGACCTACTTACAAAGTGGCATATATTGCAATTTATTTTAATTAAGATACCTATTATATATT
TCTTTATAGAAAAAGTCTGGAAGAGTTTACTTCAATTGTAGCAATGTGAGGTGGTGGCAGTAT
AGGTGATTTTTCTTTTAAATCTGTTAATTTATCTGTATTTCTAATTTTTCTACAATGAAGATGA
ATTCTTGTATAAAAAATAAGAAAAAGAAATTAATCTTGAGGTAAGCAGAGCAGACATCATCTCTGA
TTGTCTCAGCCTCCACTTCCCCAGAGTAAATTCAAATGAATCGAGCTCTGCTGCTCTGGTTGG
TTGTAGTAGTGATCAGGAAACAGATCTCAGCAAAGCCACTGAGGAGGAGGCTGTGCTGAGTTTGT
GTGGCTGGAATCTCTGGGTAAGGAACCTAAAGAACAAAAATCATCTGGTAATTCTTTCTAGAAG
GATCACAGCCCCCTGGGATTCCAAGGCATTGGATCCAGTCTCTAAGAAGGCTGCTGTACTGGTTGA
ATTGTGTCCCCCTCAAATTCACATCCTTCTTGGAACTCTCAGTCTGTGAGTTTATTGGAGATAAG
GTCTCTGCAGATGTAGTTAGTTAAGACAAGGTCATGCTGGATGAAGGTAGACCTAAATTCAATAT
GACTGGTTTTCTTGTATGAAAAGGAGAGGACACAGAGACAGAGGAGACGCGGGGAAGACTATGTA
AAGATGAAGGCAGAGATCGGAGTTTTCAGCCACAAGCTAAGAAACACCAAGGATTGTGGCAACC
ATCAGAAGCTTGGAAGAGGCAAGAAGAAATCTTCCCTAGAGGCTTTAGAGGGATAACGGCTCTG
CTGAAACCTTAATCTCAGACTTCCAGCCTCCTGAACGAAGAAAGAAATAAATTTCCGGCTGTTTTAA
GCCACCAAGGATAATTGGTTACAGCAGCTCTAGGAACTAATACAGCTGCTAAAATGATCCCTGT
CTCCTCGTGTGTACATTCTGTGTGTGTCCCCTCCCACAATGTACCAAAGTTGTCTTTGTGACCAA
TAGAATATGGCAGAAGTGATGGCATGCCACTTCCAAGATTAGGTTATAAAGACACTGCAGCTTC
TACTTGAGCCCTCTCTCTGCCCCACCCGCCCAATCTATCTTGGCTCACTCGCTCTGGGGG
AAGCTAGCTGCCATGCTATGAGCAGGCCTATAAAGAGACTTACGTGGTAAAAAATGAAGTCTCCT
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTTGTGTTTT
AAGTTGCTCAGTTTTGGTCTAAGTTGTATGCAGCAATAGATAAATAATATGCAGAGAAAGAG

FIGURE 152

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEESISVVPNRWLDASLSPVILGVQGG
QCLSCGVGQEPTLTLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP
VRLTQLPENGGWNAIPITDFYFQQCD

N-myristoylation sites.

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

Interleukin-1 signature.

amino acids 111-131

Interleukin-1 proteins.

amino acids 8-29, 83-120, 95-134, 64-103

FIGURE 153

CTTCAGAACAGGTTCTCCTTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC
CCTGCAGAAATCTGTGAGCTCTTTCCTTATGGGGACCCTGGCCACCAGCTGCCTCCTTCTTGG
CCCTCTTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCCAGCTGAGGCTTGACAAGTCCAAC
TTCCAGCAGCCCTATATCACCACCCGACCTTCATGCTGGCTAAGGAGGCTAGCTTGGCTGATAA
CAACACAGACGTTTCGTCTCATTGGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT
ATCTGATGAAGCAGGTGCTGAACTTCACCCTTGAAGAAGTGTGTTCCCTCAATCTGATAGGTTT
CAGCCTTATATGCAGGAGGTGGTGGCCTTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTAAAAAGC
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTTATGTCTCTGAGAAAT
GCCTGCATTTCAGCAGAGCAAAGCTGAAAAATGAATAACTAACCCCTTCCCTGCTAGAAATAA
CAATTAGATGCCCCAAAGCGATTTTTTTTAACCAAAGGAAGATGGGAAGCCAACTCCATCATG
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTTGTATTATA
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTTATTGATAACATTTTCATTGTAACTGGTGTTT
TATACACAGAAAACAATTTATTTTTTAAATAATTGTCTTTTCCATAAAAAAGATTACTTTCCAT
TCCTTTAGGGGAAAAAACCCCTAAATAGCTTCATGTTTCCATAATCAGTACTTTATATTTATAAA
TGTATTTATTATATTATAAGACTGCATTTTATTATATCATTTTATTAATATGGATTTATTAT
AGAAACATCATTCGATATTGCTACTTGAGTGTAAGGCTAATATTGATATTTATGACAATAATTAT
AGAGCTATAACATGTTTATTTGACCTCAATAAACACTTGGATATCCC

FIGURE 154

MAALQKSVSSFLMGTLATSCLLLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL
ADNNTDVRLIGEKLFHGVSMSERCYLMKQVLNFTLEEVLPQSDRFQPYMQEVVPFLARLSNRLS
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

Important features of the protein:

Signal peptide:

amino acids 1-33

N-glycosylation sites.

amino acids 54-58, 68-72, 97-101

N-myristoylation sites.

amino acids 14-20, 82-88

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 10-21

FIGURE 155

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT
CAGTCAGTGCCCGACTTGTGACTGAGTGTGCAGTGCCAGCATGTACCAGGTCAGTGCAGAGGGC
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGC
TGCCAGGTTTGGGGCTGGGGGCCAAGTGGAGTGAGAACTGGGATCCCAGGGGGAGGGTGCAGAT
GAGGGAGCGACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTTTCCTACAGGTGGTTGCAT
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCCAGTGCTGCCCCAGCAAAGGG
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCCTAGAGCCTGCTAG
GCCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTCAACAGCAGGGCCATCT
CCCCCTGGAGATATGAGTTGGACAGAGACTTGAACCGGCTCCCCAGGACCTGTACCACGCCCCGT
TGCCTGTGCCCGCACTGCGTCAGCCTACAGACAGGCTCCCACATGGACCCCCGGGGCAACTCGGA
GCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCAGCCACA
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTTAGCTTGTGTGTGTGCGGCCCCGT
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTTGGGAAACCTGGAGCCAGGTGTACA
ACCACTTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCTGTGAAGTGTGTCTGGAGCAG
CAGGATCCCGGGACAGGATGGGGGGCTTGGGGAAAACCTGCACTTCTGCACATTTGAAAAGAG
CAGCTGCTGCTTAGGGCCGCCGAAGCTGGTGTCTGTCAATTTCTCTCAGGAAAGGTTTTCAA
GTTCTGCCCATTCTGGAGGCCACCACTCCTGTCTCTTCCTCTTTTCCCATCCCCTGCTACCCCTG
GCCAGCACAGGCACTTTCTAGATATTTCCCCCTTGCTGGAGAAGAAAGAGCCCCTGTTTATT
TGTTTGTCTTACTCATCACTCAGTGAGCATCTACTTTGGGTGCATTCTAGTGTAGTTACTAGTCTT
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTTATCCAAATAAATAT
CTTTATTTAAAAATGAAAAA

FIGURE 156

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPA
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Important features of the protein:

Signal peptide:

amino acids 1-32

N-glycosylation site.

amino acids 136-140

Tyrosine kinase phosphorylation site.

amino acids 127-135

N-myristoylation sites.

amino acids 44-50, 150-156

FIGURE 157

CCGGCGATGTCGCTCGTGTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC
GACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGTACAACATGATCTAATCC
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCA
ATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA
GATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGG
CCTTCCAGACTCAGACCAGACCCCTCTGGTGGTAAATGGACATTTTCTACATCGGCTTCCCTGTA
GAGCTGAACACAGTCTATTTCAATGGGGCCCAATATTCCTAATGCAAATATGAATGAAGATGG
CCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATAATGAAATATAAAAAA
AGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGTGAAGAAGATGAGGAGACA
GTAGAAGTGAATTCACAACCACTCCCTTGGGAAACAGATACATGGCTCTTATCCAACACAGCAC
TATCATCGGGTTTTCTCAGGTGTTTGGCCACACCAGAAGAAACAAACGCGAGCTTCAGTGGTGA
TTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGC
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTTCCCTCT
GGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCCTCTCTCTGCTGTCTCTGCTGGTGGCA
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTT
TCTACCACCACACTACTGCCCCCATTAAGGTCTTGTGGTTTACCCATCTGAAATATGTTTCCA
TCACACAATTTGTTACTTCACTGAATTTCTTCAAACCATTCAGAAAGTGAGGTCATCCTTGAAA
AGTGGCAGAAAAAGAAAATAGCAGAGATGGGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCA
GCAGACAAAGTCGTCTTCTTCTTTCCAATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAA
GAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCCCTTGCCTTAACCTTTTCTGCA
GTGATCTAAGAAGCCAGATTCATCTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACA
AAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTT
CTGTGCAGAACTTCTCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAAGCCTGCCACG
ATGGCTGCTGCTCCTTGTAG

FIGURE 158

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRLDLRVEPVTTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNF TSPGCLDHIMYKKKCKVAGSLWDPNITACKKNEETVEVNF TTTPLGNRYMALIQH
STIIGFSQVFEPHQKQTRASVVIPTVDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPTGVPFPLDNNK
SKPGGWLP LLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHV KQVVSAGKRSQACHD
GCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283
- 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 159

AGCCACCAGCGCAACCATGACAGTGAAGACCCCTGCATGGCCCAGCCATGGTCAAGTACTTGCTGCT
GTCGATATTGGGGCTTGCCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA
CTTTTTTCCAAAAGCCTGAGAGTTGCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC
ATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGA
ACTTGGGCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAA
GAGACCCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTTCTTCCAGTTGGAGAAGGTGCT
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCC
ACTCAGCTGAAGAAG

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FIGURE 160

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVMSRNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQ GKEDISMNSVPIQQETLVV
RRKHQGC SVSFQLEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

amino acids 1-30

N-glycosylation site.

amino acids 83-87

N-myristoylation sites.

amino acids 106-111, 136-141

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINEN
QRVMSRNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQ GKEDISMNSVPIQQETLVV
RRKHQGC SVSFQLEKVLVTVGCTCVTPVIHHVQ

FIGURE 161

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 A C A G A G A G T G C A C A A A C T A C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G A T T C
 C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C T T G G G G G G G G C A G C A C
 A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T C C C T G T G C C C T G G T T C T T G C T G T C C T
 T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A G G A C G T A C C
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 G A A G A G C C T G A A G A T G A G G A A A A G T T T G G A G G A G C A G C T G A C T C A G G G G T G G A G G A G C C T A G G A A
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 T G G A G G T G C A A G T G C C T G C C C T T G T G C A G T T T G G T C A G T C T G T G G G C T C T G T G G T A T A T G A C
 T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C C T A T A C T C A G C C C A G G T A C G A G A A
 G G A A C T C A A C C A C A C A C A G C A G C T G C C T G C C C T G C C C T G G C T C A A C G T G T C A G C A G A T G G T G A C A
 A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A C T T C G G C C T C T C C C T G A C T G G A A T C A G
 G T C C A G G G C C C C C A A A A C C C G G T G G C A C A A A A A C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A
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 C G A T G T G C T A C T G T T G G A G A C A C G A G G C C C C A G G A C A C A G A T C C C C T C T G T G C C T T G G A A C C C A
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 C C G T A G A C C T G T G G A G C C G T C G T G A A C T G A G C G C G A G G G C C C G T G G C T T G G T T T C A C G C G C A G
 C G G C G C C A G A C C C T G C A G A G G G C G G C G T G G T G G T C T T G C T C T T C T C T C C C G G T G C G G T G G C G C T
 G T G C A G C G A G T G G C T A C A G G A T G G G G T G T C C G G G C C G G G G C G C A C G G C C C G C A C G C C T C C
 G C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G G
 G C C T G C T T C G A C A G G C T G C T C C A C C G G A C G C C G T A C C C G C C C T T T C C G C A C C G T G C C C G T C T T
 C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G T T C C G
 G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G C T A C T T C
 C A T C C C C C G G G A C T C C C G C G C C G G A C G C G G G T G G G A C C A G G G C G G G A C C T G G G G C G G G G A
 C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T T C T A A A A A A A

FIGURE 162

MPVPWFLLSLALGRSPVVLRLVGPQDATHCS PGLSCRLWDS DILCLPGDIVPAPGPVLA PTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
QVPAALVQFGQSVGVSVDCEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNV SADGDNVHLVNLVS
EEQHFGLSLYWNQVQGPPKPRWHKNLTG PQIITL NHTDLVPCLCIQVWPLEPDSVRTNICPFRED PRAHQN
LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFP LLKGHPNLCVQ
VNSSEKIQEQECLWADSLGPLKDDVLLLETRGPQDNRSICALEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSGAAARG
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAFWHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGFGAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRL LHPPDAVPALFRTVPVFT
LPSQLPDFLGALQQPRAPRSGRLQERAEQVSRAIQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

Signal sequence:

amino acids 1-20

Transmembrane domain.

amino acids 453-475

N-glycosylation sites.

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,
334-337, 357-360, 391-394

Glycosaminoglycan attachment site.

amino acids 583-586

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 552-555

N-myristoylation sites.

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,
692-697, 696-701, 700-705

FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCGATGAGGACGCTGCTGACCATCTTGACTGTGGGATCCCTGGCT
 GCTCACGCCCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCAGTCCAGCAACTTTGA
 AAACATCCTGACGTGGGACAGCGGGCCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA
 AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGCGGATCACCCGGAAGTCCTGC
 AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTCACCGCT
 GTCAGTGC GGAGGCGGTCAGCCACCAAGATGACTGACAGGTTGAGCTCTCTGCAGCACACTAC
 CCTCAAGCCACCTGATGTGACCTGTATCTCCAAAGTGAGATCGATTGAGATGATTGTTTCATCCTA
 CCCCCACGCCAATCCGTGCAGGCGATGGCCACCGGCTAACCTTGGAGACATCTTCCATGACCTG
 TTCTACCACTTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAGCAGAGAGA
 ATATGAGTTCTTCGGCCTGACCCCTGACACAGAGTTCCTTGGCACCATCATGATTGCGTTCCCA
 CCTGGGCCAAGGAGAGTGGCCCTACATGTGCCGAGTGAAGACACTGCCAGACCGGACATGGACC
 TACTCCTTCTCCGGAGCCTTCCTGTTCTCCATGGGCTTCCTCGTCGAGTACTCTGCTACCTGAG
 CTAAGATATGTACCAAGCCGCTGCACCTCCCAACTCCCTGAACGTCCAGCGAGTCCCTGACTT
 TCCAGCCGCTGCGCTTTCATCCAGGAGCAGTCTGATCCCTGTCTTTGACCTCAGCGGCCCCAGC
 AGTCTGGCCCCAGCCTGTCCAGTACTCCAGATCAGGGTGTCTGGACCCAGGGAGCCCCGAGGAGC
 TCCACAGCGGCATAGCCTGTCCGAGATCACCTACTTAGGGCAGCCAGACATCTCCATCCTCCAGC
 CCTCCAACGTGCCACCTCCCAGATCCTCTCCCCACTGTCTATGCCCCAAACGCTGCCCCTGAG
 GTCGGGCCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCCATTCTAGCCCCACA
 GGCCATCTTAAGGTCCAGCCTTCCTCCTATGCCCCCAAGCCACTCCGGACAGCTGGCCTCCCT
 CCTATGGGGTATGCATGGAAGTTCTGGCAAAGACTCCCCACTGGGACACTTTCTAGTCTTAA
 CACCTTAGGCCTAAAGGTGAGCTTTCAGAAAGAGCCACCAGCTGGAAGCTGCATGTTAGGTGGCT
 TTCTCTGCAGGAGGTGACCTCCTTGGCTATGGAGGAATCCCAAGAAGCAAAATCATTGCACCAGC
 CCCTGGGGATTTGCACAGACAGAACATCTGACCCAAATGTGCTACACAGTGGGGAGGAAGGGACA
 CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCCTCAGTCCAGATCGAGGGCCACCCATGTC
 CCTCCCTTTGCAACCTCCTTCCGGTCCATGTTCCCCCTCGGACCAAGGTCCAAGTCCCTGGGGCC
 TGCTGGAGTCCCTTGTGTGTCCCAAGGATGAAGCCAAGAGCCAGCCCTGAGACCTCAGACCTG
 GAGCAGCCACAGAACTGGATTCTCTTTTCAGAGGCTGGCCCTGACTGTGCAGTGGGAGTCCCTG
 AGGGGAATGGGAAAGGCTTGGTGCTTCCTCCCTGTCCCTACCCAGTGTACATCCTTGGCTGTCA
 ATCCCATGCCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCCCTTGAGAGAAGC
 AGAGGGAGTGGCATGCAGGGCCCCCTGCCATGGGTGCGCTCCTCACCGGAACAAAGCAGCATGATA
 AGGACTGCAGCGGGGAGCTCTGGGGAGCAGCTTGTGTAGACAAGCGCGTGTCTGCTGAGCCCTG
 CAAGGCAGAAATGACAGTGAAGGAGGAATGCAGGGAACTCCCGAGGTCCAGAGCCCCACCTC
 CTAACACCATGGATTCAAAGTGCTCAGGGAATTTGCCTCTCCTTGGCCATTCTTGCCAGTTTC
 ACAATCTAGCTCGACAGAGCATGAGGCCCCCTGCCCTCTTCTGTGATTGTTCAAAGGTGGGAAGAGA
 GCCTGGAAAAGAACCAGGCCTGGAAAAGAACCAGAAGGAGGCTGGGCAGAACCAGAACAACCTGC
 ACTTCTGCCAAGGCCAGGGCCAGCAGGACGGCAGGACTCTAGGGAGGGGTGTGGCCTGCAGCTCA
 TTCCAGCCAGGGCACTGCCTGACGTTGCACGATTTTCAGCTTCATTCTCTGATAGAACAAAGC
 GAAATGCAGGTCCACCAGGGAGGGAGACACACAGCCTTTTCTGCAGGCAGGAGTTTCAGACCT
 ATCCTGAGAATGGGTTTGAAGGAAGGTGAGGGCTGTGGCCCTGGACGGGTACAATAACACAC
 TGTACTGATGTACAACTTTGCAAGCTCTGCCCTTGGGTTTCAGCCATCTGGGCTCAAATTCAGC
 CTCACCACTCACAAGCTGTGTGACTTCAAACAAATGAAATCAGTGCCAGAACCTCGGTTTCCTC
 ATCTGTAATGTGGGGATCATAACCTACCTCATGGAGTTGTGGTGAAGATGAAATGAAGTCATG
 TCTTTAAAGTGCTTAATAGTGCCTGCTACATGGGCAGTGCCCAATAAACGGTAGCTATTTAAAA
 AAAAAAA

FIGURE 164

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW
VAKKGCQRITRKSCNLTVETGNLTelyarvtavsaggrsatkmtDRFSSLQHTTLKPPDVTCIS
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMLGGKQREYEFFGLTPDT
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP
PNSLNVQRVLTfQPLRFIQEHVLIpVFDLSGPSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAIKVPSSY
APQATPDSWPSPSYGVCMEGSGKDSPTGTLSSPKHLRPGQLQKEPPAGSCMLGGLSLQEVTSIAM
EESQEAkslHQPLGICTDRTSDPNVLHSGEEGTPQYLKGQLPLLSSVQIEGHPMSLPLQPPSGPC
SPSDQGSPWGLLESVCPKDEAKSPAPETSDLEQPTELDSLFRGLALTQWES

Signal sequence.

amino acids 1-17

Transmembrane domain.

amino acids 233-250

N-glycosylation sites.

amino acids 80-83, 87-90, 172-175

N-myristoylation sites.

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

FIGURE 165

TGGCCTACTGGAAAAAAAAAAAAAAAAAAGTCACCCGGGCGCGGTGGCCACAACATGG
CTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTCTGCTGGGGGCGCTCTGGTGGGTCCCGGGCCAG
TCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT
GTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTGTGAATTTTA
AAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAACCTTGGGCTGGA
AGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCATAAATACACGGA
AGAAGAGCTACATATTCAGCAGATGAGACAGACTTGTCTGCTTTGAAGGAGGAAGAGATGATT
TTAATAGTTATAATGTAGAAGAGCTTTAGGATCTTTGGAAGTGGAGGACTCTGTACCTGAAGAG
TCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA
ACTTGACCCTGTGCCCTGAGCCCGAGGCATTAGAGCTGATTAGAGGATGGAGAAGGTGCTTTCT
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGAGAGCCACCCTCACACCAGCGGT
CCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACACTTTTGAAGAAATCTGCACGATAA
ATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAGTTCTCCTGCCTCGGTGGAGCGGGAGA
AGACAGATGCTTACAAAGTCTTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGCCTTATT
CATTACAGCAAAGGATTTGCTTGGCATCAAATCTAAGTTTGTTTTACAAAGATTGTTTTTAGTA
CTAAGCTGCCTTGGCAGTTTGCATTTTGTAGCCAAACAAAAATATATTATTTTCCCTTCTAAGTA
AAAAAAAAAAAAAAAAAAAA

FIGURE 166

MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD CRFVN
FKKGDDVYVYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADETD FVCFEGGRD
DFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELD PVPEPEAFRA DSEDEGEA
FSESTEG LQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNL SLFYKDCF

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34

Tyrosine kinase phosphorylation site.

amino acids 67-76

N-myristoylation sites.

amino acids 205-211, 225-231, 277-283

Amidation site.

amino acids 28-32

FIGURE 167

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCTAGAGGCCGGGGAAGAGAAGCAAAGCGC
AACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCCTAACTTC
AGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCGCGGCACAGG
CGCGGCAGGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTTCGGGCAGCTGGGCTCGGGC
GGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTCGCGGGCTGCGCCCTG
GGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCCGCGATGAGCCGCGTGG
TCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCCTTCTGCCGCGCGTGGTTCAGC
GGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGAACT
GTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTTGTGAGAGTGAGGGAGGAGTCTCTCTCA
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG
ACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGAATGGAGATGGGCAAACATCTGG
TGCCTGCCCAGATCTCTACCAAGTGGTCTGATGGAAGCAATTCACAGTACCGAAACTGGTACACAG
ATGAACCTTCCTGCGGAAGTGAAGAGTGTGTTGTGATGTATCACCACCAACTGCCAATCCTGGC
CTTGGGGGTCCCTACCTTTACCAAGTGAATGATGACAGGTGTAACATGAAGCACAATTATATTTG
CAAGTATGAACCAGAGATTAATCCAACAGCCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAG
GAGACACCCATCAGAATGTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTT
ATACCAACAATACCCCTGCTCTTACTGATACTGGTTGCTTTTGGAACCTGTTGTTTCCAGATGCT
GCATAAAAGTAAAGGAAGAACAAAACCTAGTCCAAACAGTCTACACTGTGGATTTCAAAGAGTA
CCAGAAAAGAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCAGAAATTTTGTAAATCT
GGATCTGTATAAGGAATGGCATCAGAACAATAGCTTGAATGGCTTGAAATCACAAAGGATCTGC
AAGATGAACGTGAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTATATGTCTATTATTTCA
TTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAA
ACTTCAAACCTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTA
TGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTAGTCAATGTAA
TGTATATTGTATTGAAATTTACAGTGTGCAAAAGTATTTTACCTTGCATAAGTGTGTTGATAAAA
ATGAACCTGTTCTAATATTTATTTTATGGCATCTCATTTTCAATACATGCTCTTTTGATTAAAG
AACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGT
TTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGA
AATAAGAAGCTATTTTCAATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGAT
TGTCTAATTTCAATTGTGCAAGACATGTGCCCTTATAATTATTTTGTAGCTTAAATTAACAGATT
TTGTAATAATGTAACCTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAAG
TGACATACACAATATAAATCATATGTCTTCACACGTTGCCCTATATAATGAGAAGCAGCTCTCTGA
GGGTTCTGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGG
ATTGACACTGGAGGCAGATAGTTGCAAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTG
ACTATATTAGTATACAAAGAGGTCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAG
ACAAGCACAGCACACAGACATTTTAGGAAGGAAAGGAACACGAAATCGTGTGAAATGGGTTGG
AACCCATCAGTGATCGCATATTCATTGATGAGGGTTTGGCTTGAGATAGAAAATGGTGGCTCCTTT
CTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCCTTGTCTCTTCAAGAGAAAGTTGTAACCTCT
CTGGTCTTCATATGTCCCTGTGCTCCTTTTAAACCAATAAAGAGTTCTTGTCTTGGGGGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MSRVVSLLLGAALLCGHGAFRRVVSQKVCFAFKHPCYKMAFHELSSRVSFQEARLACESE
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNKYCKYEPEINPTAPVEK
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSCKGRKTKSPNQ
STLWISKSTRKESGMEV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89, 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217